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(54) Title: ELONGATION FACTOR-2 KINASE (EF-2 KINASE) AND METHODS OF USE THEREFOR		
(57) Abstract <p>A new superfamily of protein kinases has been discovered that centers around eukaryotic elongation factor-2 kinase (eEF-2 kinase). The protein kinases of this new superfamily have the following characteristics: 1) sequence similarity to eEF-2 kinase; 2) no sequence similarity to the protein kinases of either the serine/threonine/tyrosine kinase or histidine kinase superfamily; and, 3) specifically phosphorylates α-helical regions of proteins as opposed to β-turns, as seen in all other protein kinases. Assays have been developed utilizing eEF-2 kinase and a phosphorylation target consisting of a novel α-helical 16-amino acid peptide sequence to facilitate high-throughput screening for compounds that can specifically inhibit this protein kinase that has been implicated tumor growth and other hyperproliferative disorders. Additionally, the disclosed invention includes assessing eEF-2 kinase levels for diagnostic purposes, and therapeutic formulations to inhibit eEF-2 kinase activity.</p>		

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ELONGATION FACTOR-2 KINASE (EF-2 KINASE) AND METHODS OF USE THEREFOR

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FIELD OF THE INVENTION

This invention relates generally to the identification of a new superfamily of eukaryotic protein kinases and the use of one member of this superfamily, elongation factor-2 kinase (eEF-2 kinase), in assays to screen for specific inhibitors. Specifically, this invention provides an isolated nucleic acid encoding a heart protein kinase, a melanoma
10 protein kinase and a ch4 protein kinase. Specific inhibitors of the eEF-2 kinase may be potent therapeutics for amelioration of malignant transformation. Additionally, sequences complementary to eEF-2 kinase may have therapeutic efficacy as antisense drugs or be used in gene therapy. Specifically, the invention relates to assays developed using the recombinant eEF-2 kinase to screen for inhibitors of phosphorylation of a
15 peptide derived from the myosin heavy chain (MHC) protein.

BACKGROUND OF THE INVENTION

Protein phosphorylation plays a critical role in many cellular processes (Krebs (1994) *Trends Biochem. Sci.* 19:439; Hanks and Hunter, (1996) *FASEB J.* 9:576-596; Hardie
20 and Hanks, (1995) *The Protein Kinase Facts Book* (Academic, London)). There are two well-characterized superfamilies of protein kinases, with most of the protein kinases belonging to the serine/threonine/tyrosine kinase superfamily (Hanks and Hunter, (1996); Hardie and Hanks, (1995)). The characterization of several hundred
25 members of this superfamily revealed that they all share a similar structural organization of their catalytic domains which consist of twelve conserved subdomains (Hanks and Hunter, (1996); Hardie and Hanks, (1995)). The other superfamily is referred to as the histidine kinase superfamily and is involved in the prokaryotic two-
component signal transduction system, acting as sensor components (Stock et al., (1989) *Microbiol. Rev.* 53:450-490; Parkinson and Kofoed, (1992) *Annu. Rev. Genet.*
30 26:71-112; Swanson, et al., (1994) *Trends Biochem. Sci.* 19:485-490). Recently, eukaryotic members of this superfamily have also been described (Chang et al., (1993) *Science* 263:539-544; Ota and Varshavsky, (1993) *Science* 262:566-569; Maeda et al.,

(1994) *Nature* 369:242-245). Mitochondrial protein kinases have also recently been described that show structural homology to the histidine kinases, but phosphorylate their substrates on serine (Popov et al., (1992) *J. Biol. Chem.* 267:13127-13130; Popov et al., (1993) *J. Biol. Chem.* 268:26602-22606). Finally, several new protein kinases
5 have been reported that show a lack of homology with either of the kinase superfamilies (Maru and Witte, (1991) *Cell* 67:459-468; Beeler et al., (1994) *Mol. Cell. Biol.* 14:982-988; Dikstein et al., (1996) *Cell* 84:781-790; Futey et al., (1995) *J. Biol. Chem.* 270:523-529; Eichenger et al., (1996) *EMBO J.* 15:5547-5556). However, these protein kinases are viewed as an exception to the general rule as they have yet to
10 be fully characterized.

The cloning and sequencing of the extensively characterized eukaryotic elongation factor-2 kinase (eEF-2 kinase) from a variety of eukaryotic organisms has now revealed the existence of a novel class of protein kinases (Ryazanov et al., (1997) *Proc. Natl.*
15 *Acad. Sci., USA* 94:4884-4889). eEF-2 kinase, previously known as Ca^{2+} /calmodulin-dependent protein kinase III, is highly specific for phosphorylation of elongation factor-2 (eEF-2), an abundant cytoplasmic protein that catalyzes the movement of the ribosome along mRNA during translation in eukaryotic cells (reviewed in Ryazanov and Spirin, (1993) In *Translational Regulation of Gene Expression* (Plenum, New
20 York) Vol. 2, pp. 433-455; Nairn and Palfrey, (1996) In *Translational Control* (CSHL Press, New York) pp. 295-318). All mammalian tissues, and various invertebrate organisms, exhibit eEF-2 kinase activity (Abdelmajid et al., (1993) *Int. J. Dev. Biol.* 37:279-290). eEF-2 kinase catalyzes the phosphorylation of eEF-2 at two highly conserved threonine residues located within a GTP-binding domain (Ryazanov and
25 Spirin, (1993) In *Translational Regulation of Gene Expression* (Plenum, New York) Vol. 2, pp. 433-455; Nairn and Palfrey, (1996) In *Translational Control* (CSHL Press, New York) pp. 295-318). When eEF-2 is phosphorylated, it becomes inactive with respect to protein synthesis (Ryazanov et al., (1988) *Nature* 334:170-173). Since eEF-2 phosphorylation is dependent on Ca^{2+} and calmodulin, eEF-2 kinase plays a pivotal
30 role in modulating the protein synthesis rate in response to changes in intracellular

calcium concentration. Phosphorylation of eEF-2 has also been linked to the regulation of cell cycle progression. For example, transient phosphorylation of eEF 2 occurs during the mitogenic stimulation of quiescent cells (Palfrey et al., (1987) *J. Biol. Chem.* 262:9785-9792) and during mitosis (Celis et al., (1990) *Proc. Natl. Acad. Sci., USA* 87:4231-4235). In addition, changes in the level of eEF-2 kinase activity is associated with a host of cellular processes such as cellular differentiation (End et al., (1982) *J. Biol. Chem.* 257:9223-9225; Koizumi et al., (1989) *FEBS Lett.* 253:55-58; Brady et al., (1990) *J. Neurochem.* 54:1034-1039), oogenesis (Severinov et al., (1990) *New Biol.* 2: 887-893), and malignant transformation (Bagaglio et al., (1993) *Cancer Res.* 53:2260-2264).

The sequence eEF-2 kinase appears to have no homology to either the Ca^{2+} /calmodulin-dependent protein kinases or to any members of the known protein kinase superfamilies (Ryazanov et al., (1997) *Proc. Natl. Acad. Sci., USA* 94:4884-4889). However, the recently described myosin heavy chain kinase A (MHCK A) from *Dictyostelium* (Futey et al., (1995) *J. Biol. Chem.* 270:523-529) shows a great deal of homology with eEF-2 kinase. These two kinases define a novel class of protein kinases that may represent a new superfamily.

Evidence for MHCK and eEF-2 kinase forming the core of a new superfamily is as follows. MHCK A from *Dictyostelium*, has a demonstrated role in the regulation of myosin assembly (Futey et al., (1995) *J. Biol. Chem.* 270:523-529; Côté et al., (1997) *J. Biol. Chem.* 272:6846-6849). eEF-2 kinase is a ubiquitous Ca^{2+} /calmodulin-dependant protein kinase involved in the regulation of protein synthesis by Ca^{2+} (Redpath et al., (1996) *J. Biol. Chem.* 271:17547-17554; Ryazanov et al., (1997) *Proc. Natl. Acad. Sci., USA* 94:4884-4889). Both MHCK A and eEF-2 kinase display no homology to any of the known protein kinases, but are strikingly similar to each other; amino acid sequences of their catalytic domains are 40% identical. Another protein kinase homologous to MHCK A and eEF-2 kinase has recently been identified in *Dictyostelium* (Clancy et al., (1997) *J. Biol. Chem.* 272:11812-11815), and an

expressed sequence tag (EST) sequence, with a high degree of similarity to the catalytic domain common to both MHCK A and eEF-2 kinase, has been deposited in GenBank (clone FC-AN09/accession #C22986). An amino acid sequence alignment of the catalytic domains of these new protein kinases is shown in Figure 1A. These kinases
5 have a catalytic domain of approximately 200 amino acids which can be subdivided into seven conserved subdomains. Subdomains V, VI, and VII have a predicted β -sheet structure and are presumably involved in ATP-binding, while subdomains I through IV may be involved in substrate binding and catalysis. These new protein kinases have no homology to the members of the eukaryotic serine/threonine/tyrosine protein kinase
10 superfamily with the exception of the GXGXXG motif in subdomain VI which is present in many ATP-binding proteins. Thus, MHCK A, eEF-2 kinase, and related protein kinases may represent a new superfamily. Evolutionary analysis of these new kinases (Figure 1B) reveals that they can be subdivided into 2 families: the eEF-2 kinase family which includes eEF-2 kinases from different organisms, and the MHCK
15 family which includes MHCK A, MHCK B and FC-AN09. These two families appear to have split more than a billion years ago.

An interesting question is why does nature employ these unusual kinases to phosphorylate eEF-2 and myosin heavy chains? Perhaps the answer is related to the
20 secondary structure of the phosphorylation sites. As was originally reported by Small et al. (Small et al., (1977), *Biochim. Biophys. Res. Comm.* 79:341-346), phosphorylation sites are usually located at predicted β -turns. Subsequent studies, including X-ray crystallographic data, demonstrated that phosphoacceptor sites in substrates of conventional protein kinases are often located in turns or loops and usually
25 have flexible extended conformation (Knighton et al., (1991) *Science* 253:414-420; Pinna and Ruzzene (1996) *Biochim. Biophys. Acta* 1314:191-225). In contrast to this, the existing evidence suggests that the peptides around phosphorylation sites for eEF-2 kinases and MHCK A have an α -helical conformation. The two major phosphorylation sites for MHCK A are located in a region which has a coiled-coil α -helical structure
30 (Vaillancourt et al., (1988) *J. Biol. Chem.* 253:10082-10087). The major

phosphorylation site in eEF-2, threonine 56, is located within a sequence which is homologous among all translational elongation factors. In the crystal structure of the prokaryotic elongation factor EF-Tu, this sequence has an α -helical conformation (Polekhina *et al.*, (1996) *Structure* 4:1141-1151; Abel *et al.*, (1996) *Structure* 4:1153-1159). These facts suggest that eEF-2 kinase and MHCK A differ from conventional protein kinases in that they phosphorylate amino acids located within α -helices.

Thus, in addition to the two well-characterized superfamily of eukaryotic protein kinases, which phosphorylate amino acids located in loops and turns, there appears to be a third superfamily of α -helix-directed kinases.

SUMMARY OF THE INVENTION

In accordance with the present invention, a new superfamily of protein kinases and corresponding methods for assaying their phosphorylation activity are disclosed. The protein kinases of this new superfamily have the following characteristics: 1) No significant sequence homology to protein kinases of either the serine/threonine/tyrosine kinase or histidine kinase super families; 2) moderate to high ($\geq 40\%$) to eEF-2 kinases from any organism; and, 3) phosphorylates an amino acid within an α -helical domain.

The present invention also relates to a recombinant DNA molecule or cloned gene, or a degenerate variant thereof, which encodes eEF-2 kinase; preferably a nucleic acid molecule, in particular a recombinant DNA molecule or cloned gene, encoding the eEF-2 kinase has a nucleotide sequence or is complementary to a DNA sequence shown in Figure 5 (SEQ ID NO: 1, 3, and 9).

The present invention also relates to an isolated nucleic acid molecule which encodes a heart protein kinase. The present invention also relates to an isolated nucleic acid molecule which encodes a melanoma protein kinase. The present invention also relates to an isolated nucleic acid molecule which encodes a ch4 protein kinase.

The human and murine DNA sequences of the eEF-2 kinase gene of the present invention or portions thereof, may be prepared as probes to screen for complementary sequences and genomic clones in the same or alternate species. The present invention extends to probes so prepared that may be provided for screening cDNA and genomic
5 libraries for the eEF-2 kinase gene.

The present invention also includes eEF-2 kinase proteins having the activities noted herein, and that display the amino acid sequences set forth and described above and selected from SEQ ID NO: 2, 4, and 10.

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The invention includes an assay system for screening of potential drugs effective at attenuating eEF-2 kinase activity of target mammalian cells by interrupting or potentiating the phosphorylation of eEF-2. It is a further object of the present invention to provide antibodies to the phosphorylated eEF-2 kinase target, and methods for their
15 preparation, including recombinant means.

It is a further object of the present invention to provide a method for detecting eEF-2 kinase activity in mammals in which invasive, spontaneous, or idiopathic pathological states are suspected to be present.

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It is a still further object of the present invention to provide a method for the treatment of mammals to control the amount or activity of eEF-2 kinase, so as to alter the adverse consequences of such presence or activity, or where beneficial, to enhance such activity.

25

It is a still further object of the present invention to provide a method for the treatment of mammals to control the amount or activity of eEF-2 kinase, so as to treat or avert the adverse consequences of invasive, spontaneous or idiopathic pathological states.

It is a still further object of the present invention to provide pharmaceutical compositions for use in therapeutic methods which comprise or are based upon a sequence complementary to that of the eEF-2 kinase mRNA, which would form the basis for an antisense therapeutic that can reduce expression, and thus activity, of eEF-2 kinase.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1B.

(A) Sequence alignment of the catalytic domains of human eEF-2 kinase, *C. elegans* eEF-2 kinase, MHCK A, MHCK B and clone FC-ANO9. Identical amino acids (bold) and conserved hydrophobic amino acids ("") are noted. (B). Phylogenetic tree of sequences shown in (A), with the addition of mouse and rat eEF-2 kinases. Tree was obtained using the J. Hein method with PAM250 residue weight table. The following accession numbers were used for the sequences: U93846-U93850, 1495779, 1170675, 1903458, C22986.

Figure 2. Expression of recombinant eEF-2 kinase *in vitro*. Plasmid DNA from clones *Cefk-1*, *Cefk-2*, as well as mouse and human eEF-2 kinase cDNA were used in the TNT wheat germ extract coupled transcription/translation system (Promega). [³⁵S]Methionine-labeled products were then analyzed by SDS/PAGE.

Figure 3. Activity of recombinant eEF-2 kinase *in vitro*. A large scale (0.5 ml) reaction using a mixture of *Cefk-1* and *Cefk-2* plasmids was run as in Figure 2, with the omission of labeled methionine. In the control experiment, the reaction was run with a plasmid containing a luciferase gene. (A) The reaction mixtures were separated by chromatography on a Mono Q column as described. (B) eEF-2 kinase activity in fractions was measured as the ability to phosphorylate purified rabbit eEF-2 in the

presence of [γ - 32 P]ATP. Purified rabbit reticulocyte eEF-2 kinase was used in the (+) control experiments. (C) Ca^{2+} /calmodulin-dependency of recombinant *C. elegans* eEF-2 kinase. Mono Q fraction 25 was assayed in a standard eEF-2 kinase assay in the presence and absence of Ca^{2+} and calmodulin and 20 μM trifluoperazine (TFP) or *N*-(6 aminoethyl)-5-chloro-1-naphthalene-sulfonamide (W7). (D) Ca^{2+} /calmodulin-dependency of recombinant human eEF-2 kinase. Human eEF-2 kinase cDNA was expressed in a coupled transcription/translation system as described above and eEF-2 kinase activity was assayed without further purification.

Figure 4. Northern blot analysis of tissue distribution of mouse eEF-2 kinase mRNA. Northern blots of mouse tissue containing 2 μg of polyadenylated RNA per lane were probed with the random-primed ^{32}P -labeled mouse eEF-2 kinase cDNA (31). The major transcript appeared at 3.1 kb and minor transcripts at 6.1 and 2.5 kb were also apparent (exposure time, 5 days). The same blots were stripped and rehybridized with a human eEF-2 cDNA (exposure time, 4 days).

Figure 5. Sequence alignment of *C. elegans*, mouse, human eEF-2 kinase, and the catalytic domain of *Dictyostelium discoideum* MHCK A. Identical amino acids are indicated by dark blue boxed regions and chemically conserved amino acids are indicated by light blue shaded regions. Amino acids in the human sequence that are identical to the mouse sequence are represented by dots. Amino acids underlined in black correspond to the six regions that match peptides obtained from the sequencing of purified rabbit reticulocyte eEF-2 kinase. The GXGXXG nucleotide-binding motif is underlined in red. The blue dashed line over residues 625-632 in *C. elegans* eEF-2 kinases designates the amino acids corresponding to exon 4, which is missing in *Cefk-2*.

- Figure 6. Substrate specificity of eEF-2 kinase and MHCK A. Phosphorylation assays containing eEF-2 kinase (~50 ng) or MHCK A (0.2 µg) and either 0.5 µg rabbit reticulocyte eEF-2 or 0.1 µg *Dictyostelium* myosin were performed under standard conditions except that incubation time was extended to 10 min.
- Figure 7. Schematic representation of the structure of mammalian and *C. elegans* eEF-2 kinases and MHCK A. The homologous regions are represented by dark shading. The regions of weak similarity are represented by light shading. The position of the GXGXXG motif is indicated by vertical arrows.
- Figure 8. Assay for eEF-2 kinase activity. Recombinant eEF-2 kinase (2 µg) was incubated with increasing concentrations of a peptide phosphorylation target (RKKGESEKTKKEFL) in a buffer consisting of 12.5 mM Hepes-KOH (pH 7.4), 2.5 mM magnesium acetate, 1.25 mM DTT, 25 µM CaCl₂, 0.5 µg calmodulin, 100 µM ATP, and 0.5 µCi [γ -³³P]ATP in a total volume of 50 µl. Samples were incubated at 30°C and aliquots were withdrawn at various time points, and the reaction was terminated by incubation in an ice water bath. The aliquots were then spotted onto phosphocellulose paper (2 cm x 2 cm) and washed (4 x 4 min) with 75 mM phosphoric acid. The papers were then rinsed with 100% ethanol, dried, and then counted in a scintillation counter.
- Figure 9. Sequence alignment of *C. elegans*, mouse, human eEF-2 kinase, and the catalytic domain of *Dictyostelium discoideum* MHCK A, heart kinase, melanoma kinase and ch4 kinase. Identical amino acids are indicated by dark blue boxed regions and chemically conserved amino acids are indicated by light blue shaded regions.

- Figure 10. pH-dependence of eEF-2 kinase activity: eEF-2 kinase activity was assayed by phosphorylation of the peptide substrate, MH-I at 0.2 pH unit intervals from pH 6.0-8.0.
- 5 Figure 11. Dependence of protein synthesis on intracellular pH: Protein synthesis was measured by ^3H -Leu-pulse incorporation in GH3 cells at various pH. Actual intracellular pH was determined by fluorimetric analysis.
- 10 Figure 12. Cytotoxicity assays of clones overexpressing eEF-2 kinase. MTT assays were done in quadruplicate and the results are presented as mean of values obtained.
- 15 Figure 13. Enzymatic activity of recombinant forms of human eEF-2 kinase expressed in *E. coli*. Autoradiograph of kinase assays with recombinant 6xHis-tagged eEF-2 kinase (lanes 1-4)- and GST-tagged-eEF-2 kinase (lanes 5-8). Reactions were done with and without eEF-2 (0.5 μg), and with and without calmodulin (0.5 μg). In autophosphorylation assays with 6xHis-eEF-2 kinase, 5 μg of eEF-2 kinase were used.
- 20 Figure 14. Enzymatic activity of eEF-2 kinase deletion mutants. Autoradiograph of eEF-2 kinase assay using total bacterial lysates of eEF-2 kinase deletion mutants. eEF-2 kinase assay was performed as described in text using 1 μg of total protein, and reactions were analyzed by 8% SDS-PAGE. Labels above lanes designate which amino acids are
- 25 deleted in the mutant being assayed. Deletion of amino acids 51-335 causes loss of autophosphorylation activity, and a loss of eEF-2 kinase activity. Deletion of amino acids 521-725 also causes a loss of eEF-2 kinase activity.
- 30 Figure 15. Schematic representation of wild-type and mutant eEF-2 kinases. Hatched areas represent the putative catalytic domain. Black-shaded

areas represent regions conserved between various eEF-2 kinases. White-shaded areas represent nonconserved regions. Numbers at the top of the schematic represent the amino acids at the boundaries of each of these regions. eEF-2 kinase activity and autophosphorylation activity of each mutant are summarized on the right with (+) representing presence of activity and (-) representing absence of activity. n/d = not determined

Figures 16A-16B

- 10 (A) Phosphorylation of synthetic peptides by eEF-2 kinase. See text for experimental details. X-axis = time in minutes. Y-axis = ^{33}P incorporation into peptides in counts per minute. (B) Sequences of peptides corresponding to phosphorylation site in *Dictyostelium* myosin heavy chains (MHC, MH-1) and eEF-2. Phosphoacceptor threonines are designated by an asterisk. Helical wheel representation of both peptides
- 15 is also shown. Phosphoacceptor threonines are circled.

DETAILED DESCRIPTION

Novel protein kinase inhibitors have the potential to form the basis for pharmaceutical compositions that can ameliorate malignant transformation. In order to find these inhibitors, libraries of chemical compounds are routinely screened using an automated protein kinase assay. The drawback to this approach is that most protein kinases have a very similar structure, thus making it difficult to specific inhibitors which act solely on a particular protein kinase. It was determined the primary structure of eEF-2 kinase, a ubiquitous enzyme which is involved in the regulation of protein synthesis and the cell cycle. Unexpectedly, it was found that eEF-2 kinase has a unique structure. It has no homology to any other mammalian protein kinase. This feature makes eEF-2 kinase an ideal target in the search for a specific protein kinase inhibitor. Since preliminary evidence suggests that eEF-2 kinase is upregulated in human cancers, including, but not limited to, breast cancer, identification of specific inhibitors of eEF-2 kinase can eventually lead to the development of novel anticancer drugs. In order be

able to perform a high throughput screen for an eEF-2 kinase inhibitor, it is first necessary to develop a simple assay which is amenable to automation. The existing assay involves incubation of partially purified eEF-2 kinase along with purified eEF-2 and [γ - 32 P]ATP as substrates in the presence of increasing concentrations of candidate
5 inhibitors. Results are then obtained by electrophoretic separation of the reaction mixtures, followed by autoradiography. Results are then quantified by either densitometry or scintillation counting of excised bands from the gel containing 32 P-eEF-2. Clearly, this assay, as it stands, is time-consuming, expensive, and not amenable to automation. Furthermore, it is difficult to purify large amounts of native eEF-2
10 required to perform multiple assays, and attempts to overexpress a recombinant form of eEF-2 were unsuccessful as its overexpression was toxic to host strains (personal communication from James Bodley, University of Minnesota, Minneapolis). Therefore, new methodologies for determining eEF-2 kinase activity were developed, which involves the use of a specific peptide substrate: easily and economically
15 manufactured in large scale. These methods are relatively inexpensive, fast, and can be fully automated.

In the first attempt to use a peptide as an eEF-2 kinase substrate, peptides centered around the phosphorylation site of eEF-2 were generated. This strategy did not yield
20 a peptide that was functional in phosphorylation assays. Surprisingly, it was found that a 16' mer peptide (RKKFGSEKTKTKEFL (SEQ ID NO: 20)), based on the phosphorylation site of *Dictyostelium discoideum* MHC, was an acceptable substrate for use with eEF 2 kinase in phosphorylation assays. It is interesting to note that while eEF-2 kinase can phosphorylate a peptide derived from MHC, it is not able to
25 phosphorylate native MHC (Ryazanov et al., (1997) *Proc. Natl. Acad. Sci., USA* 94:4884-4889).

In accordance with the present invention, a new superfamily of protein kinases and corresponding methods for assaying their phosphorylation activity are disclosed. The
30 protein kinases of this new superfamily have the following characteristics: 1) No

significant sequence homology to protein kinases of either the serine/threonine/tyrosine kinase or histidine kinase super families; 2) moderate to high ($\geq 40\%$) to eEF-2 kinases from any organism; and, 3) phosphorylates an amino acid within an α -helical domain.

- 5 The present invention also relates to a recombinant DNA molecule or cloned gene, or a degenerate variant thereof, which encodes eEF-2 kinase; preferably a nucleic acid molecule, in particular a recombinant DNA molecule or cloned gene, encoding the eEF-2 kinase has a nucleotide sequence or is complementary to a DNA sequence shown in Figure 5 (SEQ ID NO: 1, 3, and 9).

10

The human and murine DNA sequences of the eEF-2 kinase gene of the present invention or portions thereof, may be prepared as probes to screen for complementary sequences and genomic clones in the same or alternate species. The present invention extends to probes so prepared that may be provided for screening cDNA and genomic
15 libraries for the eEF-2 kinase gene. For example, the probes may be prepared with a variety of known vectors, such as the phage λ vector. The present invention also includes the preparation of plasmids including such vectors, and the use of the DNA sequences to construct vectors expressing antisense RNA or ribozymes which would attack the mRNAs of any or all of the DNA sequences set forth in FIGURES 5 (SEQ
20 ID NO: 1, 3, and 9). Correspondingly, the preparation of antisense RNA and ribozymes are included herein.

The present invention also includes eEF-2 kinase proteins having the activities noted herein, and that display the amino acid sequences set forth and described above and
25 selected from SEQ ID NO: 2, 4, and 10.

This invention provides an isolated nucleic acid which encodes a heart protein kinase, including analogs, fragments, variants, and mutants, thereof. In one embodiment the nucleic acid has a nucleotide sequence having at least 90% similarity with the nucleic
30 acid coding sequence as shown in Figure 9. In one embodiment the nucleic acid has a

nucleotide sequence having at least 85% similarity with the nucleic acid coding sequence as shown in Figure 9. In one embodiment the nucleic acid has a nucleotide sequence having at least 80% similarity with the nucleic acid coding sequence as shown in Figure 9. In another embodiment the nucleic acid has the following sequence:

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5  CACTTGACTGCAGGGATAAAGAAGAAAATTCTATCCAGGGTCGC
   AGCCCTGAGACTGAGGCTGGAGGAAAAGGAAAATTCGAGGAAG
   AACTCCATCGTGAAGAAGACACCTAAGTTTGAAAGGTCCTTATC
   CCGCACTGATGAGAAAAGAGACCCCAAAAGGGGCCCTTGCAAA
   GCTGAAGGGGAAAGCTCCAGTATTGCTGAAGAGGATCCAGGCCGA
10  GATGGCTCCCGAGCACTCCGGAAATATAAAGTTGAGCTGCCAGTTT TCAGA
   AATCCATGAAGACTCTACCGTCTGCTGGACAAAAGATTCCAAGTCGATAG
   CCCAGGCCAAGAAAAGCGCAGGGGACAACCTCCAGTGTTTCCTTGGCCATC
   GTCCAAGCTGGTCAGAAGGACCAGGGCCTGTATTACTGCTGCCTCAAGAA
   CAGTTATGGAAAAGTCACTGCTGAGTTTAAACCTCACAGCTGAAGTTCTCAA
15  ACAGCTTTCAAGTCACCAGAATACTAGAGGATGTGAAGAGATTGAATTCA
   GCCAGCTCATCTTCAAAGAAGATGTTTTCAATGACAGCTACTTCGGGGAC
   CACCTACGTGGCCAGATCTCCACGGAGGAGCTTCACTTTGGCGAAGGGGT
   GCACCGCAAAGCTTTCCGGAGCAAGGTGATGCAGGGCCTCATGCCGGTCT
   TCCAGCCCCGGCCACGCATGCGTACTCAAGGTGCACAATGCCGTCGCCCAT
20  GGGACCAGAAACAATGACGAACCTTGTGCAGAGGAACTACAACTGGCTG
   CCCAGGAATGCTACGTGCAGAATACTGCCAGATACTACGCCAAGATCTAC
   GCCGCTGAAGCACAGCCTCTGGAAGGCTTCGGAGAGGTGCCGGAGATCAT
   TCCTATTTTCCTTATCCATCGGCCCGAGAACAACATCCCATATGCCACAGT
   GGAAGAAGAGCTGATTGGAGAATTCGTGAAGTATTCATCCGGGACGGGA
25  AGGAAATCAACTTCCTCAGACGAGATTCAGAGGCTGGCCAGAAATGTTGC
   ACCTTCAGCACTGGGTATACCAGAAAACAAGTGGCTGTCTCCTGGTSAC
   GGACATGCAGGGTGTGGGAATGAAGTTAACTGACGTTGGCATAGCAACAC
   TAGCTAGAGGGTACAAAGGATTTAAGGGCAACTGTTCCATGACCTTCATT
   GATCAGTTCAGAGCGCTGCATCAGTGTAACAAGTACTGTAAATGCTGGG
30  GCTGAAATCCCTTCAAAACAACAGCCAGAAGCCCAGGAAGCCCATCGTCG
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GGAAAGGCAGGGTTCCGACAAACGCCACGCAGGTGAAGACGCCTGAGTC
TGAGACGCCGCCCGCAGAAAGAAAAACCTAGCCTCCCTCCTCCCTTCATC
ACCAGTGACCACCAAGCCAGCATCGCGCAGGCTTGCGCGTGGACATCTGC
AAGCACACAAGGGACACGAGCCTGCAGCCTGCAGCCGAGTGCCAGTCCTC
5 TCAGCTCCTATCACTGGCTGTCTGCTGAAAATGACAATGGCATGGCTCTTCC
AGACTAGCCTTGTAGAGAGACTTAGCAGTTCTGTTGATGCTCTCAAAGGC
AGCCCACTGTTTGTGTACACAGCTAGCCTTTCTACACACACCCTCCCCTCC
CACCGCATCGTCTATCTATCTGTGIGTCGCGCGTGGTTTGTTGACAAGAGT
TCCCCCGCTGCCCTTGGCGACTGGCCACTGTCAAAATCCTTCCCACCTCGAC
10 CCCCTCACCTCAGGATGTTCCCTGCAGTCAATGAATGTCAAGTTGTTGTTATC
AGTGTACACCGACGCTATTGTTGCTGGAGGCGGCTTCCCAGATGCGAGCCC
ATTTCCCGCCACTACCCACGCAGCCTGGCACAGTGTTCTGTTTCATTAAAT
TCATATTTAAGCAAAAAAAAAAAAAAAAAAAAAA

15 This invention provides a heart protein kinase which has the amino acid sequence as follows:

HLTAGIKKKILSRVAALRLRLEEKENSARKNSIVKKTPKFERSLSRTDEKRDPKR
APCKAEGKAPVLLKRIQAEMAPEHISGNIKLSCQFSEIHEDSTVCWTKDSKSIA
QAKKSAGDNSSVSLAIVQAGQKDQGLYYCCLKNSYGKVTAEFNLTAEVLKQ
20 LSSHQNTRGCEEIEFSQLIFKEDVFND SYFGDHLRGQISTEELHFGEVHRKAF
RSKVMQGLMPVFQPGHACVLKVIINAVAHGTRNDELVQRNYKLAAQECY
VQNTARYYAKIYAAEAQPLEGFGEVPEIPIFLHRPENNIPYATVEEELIGEFV
KYSIRDGKEINFLRRDSEAGQKCCTFQHWVYQKTSGCLLVTD MQGVGMKLT
DVGIATLARGYKGFKGNC SMTFIDQFRALHQC NK YCKMLGLKSLQNNSQKP
25 RKPIVGKGRVPTNATQVKTPESETPPAERKT

This invention provides an isolated nucleic acid which encodes a melanoma protein kinase, including analogs, fragments, variants, and mutants, thereof. In one embodiment the nucleic acid has a nucleotide sequence having at least 90% similarity with the nucleic acid coding sequence as shown in Figure 9. In one embodiment the nucleic acid has a
30

nucleotide sequence having at least 85% similarity with the nucleic acid coding sequence as shown in Figure 9. In one embodiment the nucleic acid has a nucleotide sequence having at least 80% similarity with the nucleic acid coding sequence as shown in Figure 9. On another embodiment the melanoma kinase has the following sequence:

- 5 GGCACGAGCTCGTCCACATATTACTATTATTCAGCTGTGGAAAGAAATAAC
CTGATGAGGTTGTCACAGAGTATTCCTTCGTTCTGTACCTCCACGAGGCG
GCCTGTCACAGTGTCCCGTCTGGAGGAGAGTTCTCCCAGTATACTGAATA
ACAGCATGTCTTCATGGTCTCAGCTAGGCCTCTGTGCCAAAATTGAGTTTT
TAAGTAAAGAGGAAATGGGAGGCGGTTTACGAAGAGCAGTCAAAGTGCT
10 GTGTACCTGGTCAGAGCACGATATCCTGAAGTCAGGGCATCTCTATATCAT
TAAGTCATTTCTTCCTGAGGTGATAAACACATGGTCAAGCATTATATAAGA
AGATACGGTTCTACATCTCTGTCTCAGAGAAATACAACAACAGAGAGCAG
CACAAAAGCTCACATTTGCCTTTAATCAGATGAAACCCAAATCCATACCA
TATTCTCCAAGGTTTCCTTGAAGTTTTCCTGTTGTACTGCCATTTCAGCAGGG
15 CAGTGGTTCGCTGTAGAAGAGTGCATGACTGGTGAATTIAGAAAATACAA
CAACAATAATGGTGATGAAATCATTCTTACAAATACTCTAGAAGAGATCA
TGCTAGCCTTTAGCCACTGGACCTATGAATATACCAGAGGGGAGTACTG
GTACTTGACTTACAAGGAGTGGGAGAAAACCTTGACTGACCCATCTGTAAT
AAAAGCTGAAGAAAAAAGATCCTGTGACATGGTTTTTGGCCCTGCCAATC
20 TAGGAGAAGATGCAATAAAAAACTTCAGAGCCAAACATCACTGTAATTCT
TGCTGTCGAAAGCTTAAACTTCCAGATTTGAAGAGGAATGACTACACGCC
TGATAAAATTATATTTCTCAGGATGAGTCATCAGATTTGAATCTTCAATC
TGGAATTCCACCAAAGAATCAGAAGCAACAAATTCTGTTCGTCTGATGTTA
25 This invention provides a melanoma kinase protein which has the sequence as follows:
GTSSSTYYYYSAVERNLMRLS QSIPFVPVPPRGEPVTVSRLEE SPSILNNSM
SSWSQLGLCAKIEFLSKEEMGGGLRRVAVKLCTWSEHDILKSGHLYI KSFLE
VINTWSSIYKEDTVLHLCLREIQQR AAQKLTF AFNQMKPKSIPYSPRFLEVFL
LYCHSAGQWFVFE CMTGEFRKYNNNNGDEI IPTNTLEEIMLAFSHWTYEYT
30 RGELLVLDLQGVGENLTDPSVIKATEKRSCDMVFGPANLGEDAIKNFRAKHHC

NSCCRKLKLPDLKRNDYTPDKHFPQDESSDILNLQSGNSTKESEATNSVRLML.

This invention provides an isolated nucleic acid which encodes a ch4 protein kinase, including analogs, fragments, variants, and mutants, thereof. In one embodiment the nucleic acid has a nucleotide sequence having at least 90% similarity with the nucleic acid coding sequence as shown in Figure 9. In one embodiment the nucleic acid has a nucleotide sequence having at least 85% similarity with the nucleic acid coding sequence as shown in Figure 9. In one embodiment the nucleic acid has a nucleotide sequence having at least 80% similarity with the nucleic acid coding sequence as shown in Figure 9. In another embodiment the ch 4 kinase has a nucleic acid which encodes the following amino acid sequence:

MCRKRTRARTSAAEASLRASILARDCAAAAAIIVFLVDRFLYGLDVSGKLLQV
KGLHKLQPATPIAPQVVIRQARISVNSGKLLKAEYILSSLISNNGATGTWLYRN
ESDKVLVQSVCIQIRGQILQKLGMWYEAELIWASIVGYLALPQPDKKGLSTS
15 LGILADIFVSMKNDYEKFKNNPQINLLSLKIEFDHLLSAAEACKLAAAFSA
YTPLFVLTAVNIRGTCLLSYSSSNDCCPELKNLHLCEAKEAFEIGLLTKRDDEP
VTGKQELHSFVKAAGLTTVHRRHLHGETGTVHAASQLCKEAMGKLYNFSTSSR
SQDREALSQEVMSVIAQVKEHLQVQSFSNVDDRSYVPESFECRLDKLILHGGQDF
QKILDTYSQHHTSVCEVFESDCGNNKNEQKDAKTGVCITALKTEIKNIDTVST
20 TQEKPHCQRDTGISSSLMGKNVQREILRRGGRRNWTHSDAFRVSLDQDVETET
EPSDYSNGEGAVFNKSLSGSQTSSAWSNLSGFSSSASWEEVNYHVDDRSARK
EPGKEHLVDTQCSTALSEELENDREGRAMHSLHSQLIIDLSLQEPNNDNLEPS
QNQPQQQMPLTPFSPHNTPGIFLAPGAGLLEGAPEGIQEVRNMGPRNTSAHSR
PSYRSASWSSDSGRPKNMGTIIPSVQKEEAFEIIVEFPETNCDVKDRQGKEQGE
25 EISERGAGPTFKASPSWVDPEGETAESTEDAPLDFHRVLIHNSLGNISMLPCSSF
TPNWPVQNPDSRKSGGPVAAEQGIDPDASTVDEEGQLLDSMDVPCTNGHGSH
RLCILRQPPGQRAETPNSSVSGNILFPVLSEDCITTEEGNQPGNMILNCSQNSSS
SSVWWLKSPAFFSSGSSEGDSPWSYLNSSGSSWVSLPGKMRKEILEARTLQPD
DFEKLLAGVRHDWLFQRLNTGVFKPSQLHRAHSILKYSKKSELWIAQETI
30 VYILGDYLTVKKKGRQRNAFWVHHLHQEEILGRYVGKDYKEQKGLWHHFTD

VERQMTAQHIYVTEFNKRLYEQNIPTQIFYIPSTILLILEDKTIKGCISVEPYILGE
FVKLSNNTKVVKTIEYKATEYGLAYGHFSYEFNSHIRDVVVDLQGWVTGNGK
GLIYLTDPQIHSVDQKVFTTNFGKRGIFYFFNNQHVECNEICHRLSLTRPSMEKPX

- 5 In a further embodiment of the invention, the full DNA sequence of the recombinant DNA molecule or cloned gene so determined may be operatively linked to an expression control sequence which may be introduced into an appropriate host. The invention accordingly extends to unicellular hosts transformed with the cloned gene or recombinant DNA molecule comprising a DNA sequence encoding eEF-2 kinase, and
10 more particularly, the complete DNA sequence determined from the sequences set forth above and in SEQ ID NO: 1, 3, and 9.

According to other preferred features of certain preferred embodiments of the present invention, a recombinant expression system is provided to produce biologically active
15 animal or human eEF-2 kinase.

The present invention naturally contemplates several means for preparation of eEF-2 kinase, including as illustrated herein known recombinant techniques, and the invention is accordingly intended to cover such synthetic preparations within its scope. The
20 isolation of the cDNA and amino acid sequences disclosed herein facilitates the production of eEF-2 kinase by such recombinant techniques, and accordingly, the invention extends to expression vectors prepared from the disclosed DNA sequences for expression in host systems by recombinant DNA techniques, and to the resulting transformed hosts.

25

The invention includes an assay system for screening of potential drugs effective at attenuating eEF-2 kinase activity of target mammalian cells by interrupting or potentiating the phosphorylation of eEF-2. In one instance, the test drug could be administered to a cellular sample along with ATP carrying a detectable label on its γ -
30 phosphate that gets transferred to eEF 2, or a peptide substrate, by eEF-2 kinase.

Quantification of the labeled eEF-2 or peptide substrate is diagnostic of the candidate drug's efficacy. A further embodiment would provide for the assay to be performed using a purely *in vitro* system comprised of eEF-2 kinase, ATP or labeled ATP, eEF-2 or peptide analog of a portion of eEF-2 or MHC, appropriate buffer, and detection
5 reagents and/or instrumentation to detect and quantify the extent of eEF-2 kinase-directed phosphorylation activity..

The assay system could more importantly be adapted to identify drugs or other entities that are capable of binding to the eEF-2 kinase and/or its cognate phosphorylation
10 target (e.g. eEF-2), either in the cytoplasm or in the nucleus, thereby inhibiting or potentiating eEF-2 kinase activity and its resultant phenotypic outcome. Such an assay would be useful in the development of drugs that would be specific against particular cellular activity, or that would potentiate such activity, in time or in level of activity. For example, such drugs might be used to treat various carcinomas or other
15 hyperproliferative pathologies.

The present invention likewise extends to antibodies against specifically phosphorylated eEF-2 kinase targets (e.g. eEF-2 or peptide), including naturally raised and recombinantly prepared antibodies. These antibodies and their labeled counterparts are
20 included within the scope of the present invention for their particular ability in detecting eEF-2 kinase activity *via* detection of the phosphorylated product by ELISA or any other immunoassay known to the skilled artisan.

In the instance where a radioactive label, such as the isotopes ^3H , ^{14}C , ^{32}P , ^{33}P , ^{35}S ,
25 ^{36}Cl , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{90}Y , ^{125}I , ^{131}I , and ^{186}Re are used, known currently available counting procedures may be utilized. In the instance where the label is an enzyme, detection may be accomplished by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques known in the art.

In a further embodiment, the present invention contemplates antagonists of the activity of eEF-2 kinase. In particular, an agent or molecule that inhibits phosphorylation of eEF-2. In a specific embodiment, the antagonist can be a peptide comprising sequences, or sequence variants adjacent to, and including, the phosphorylation site in
5 either eEF-2 or MHC. It is anticipated that these peptides would be competitive inhibitors of eEF-2 kinase's cognate target.

In still a further embodiment, the invention contemplates antisense drugs such that sequences complementary to the eEF-2 kinase mRNA inhibit production of functional eEF-2 kinase. In a specific embodiment, the antisense drug may be a complementary
10 oligonucleotide (DNA, RNA, or hybrid thereof), which may or may not be modified so as to have the following characteristics: 1) enhanced hybridization kinetics; 2) tighter binding to complementary sequence than its unmodified counterpart; and/or, 3) resistance to nucleases. In another specific embodiment, the antisense drug may be a complementary oligonucleotide (DNA, RNA, or hybrid thereof), that has the ability to
15 cleave its target sequence either by ribozyme, or ribozyme-like, activity, or by nuclease activity imparted on the antisense drug by physical attachment to anyone of a number of nucleases.

More specifically, the therapeutic method generally referred to herein could include the
20 method for the treatment of various pathologies or other cellular dysfunctions and derangements by the administration of pharmaceutical compositions that may comprise effective inhibitors of eEF-2 kinase activity, or other equally effective drugs developed for instance by a drug screening assay prepared and used in accordance with a further aspect of the present invention.

25

Accordingly, it is a principal object of the present invention to provide a method and an associated assay system for screening potential inhibitors of eEF-2 kinase activity.

It is a further object of the present invention to provide antibodies to the phosphorylated
30 eEF-2 kinase target, and methods for their preparation, including recombinant means.

It is a further object of the present invention to provide a method for detecting eEF-2 kinase activity in mammals in which invasive, spontaneous, or idiopathic pathological states are suspected to be present.

5 It is a still further object of the present invention to provide a method for the treatment of mammals to control the amount or activity of eEF-2 kinase, so as to alter the adverse consequences of such presence or activity, or where beneficial, to enhance such activity.

10 It is a still further object of the present invention to provide a method for the treatment of mammals to control the amount or activity of eEF-2 kinase, so as to treat or avert the adverse consequences of invasive, spontaneous or idiopathic pathological states.

15 It is a still further object of the present invention to provide pharmaceutical compositions for use in therapeutic methods which comprise or are based upon a sequence complementary to that of the eEF-2 kinase mRNA, which would form the basis for an antisense therapeutic that can reduce expression, and thus activity, of eEF-2 kinase.

20 It is yet another object of the invention to provide pharmaceutical compositions for use in therapeutic methods which comprise or are based upon peptide analogs of eEF-2 phosphorylation target amino acid sequences. It is anticipated that certain peptide analogs may act as efficacious competitive inhibitors of eEF-2 phosphorylation.

25 In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Sambrook et al. "Molecular Cloning: A Laboratory Manual" (1989); "Current Protocols in Molecular Biology" Volumes I-III [Ausubel, R. M., ed. (1994)]; "Cell Biology: A Laboratory Handbook" Volumes I-III [J. E. Celis, ed. (1994)]; "Current Protocols in Immunology" Volumes I-
30

- III [Coligan, J. E., ed. (1994)]; "Oligonucleotide Synthesis" (M.J. Gait ed. 1984);
"Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription
And Translation" [B.D. Hames & S.J. Higgins, eds. (1984)]; "Animal Cell Culture" [R.L.
Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press. (1986)]; B. Perbal,
5 "A Practical Guide To Molecular Cloning" (1984).

Therefore, if appearing herein, the following terms shall have the definitions set out below.

- 10 The terms "elongation factor-2 kinase", "eEF-2 kinase", "EF-2 kinase", "Cefk", and any variants not specifically listed, may be used herein interchangeably, and as used throughout the present application and claims refer to proteinaceous material including single or multiple proteins, and extends to those proteins having the amino acid sequence data described herein and presented in FIGURES 1 and 5 (SEQ ID NO: 2, 4, 6, 8, 10, 12,
15 abd 14), and the profile of activities set forth herein and in the Claims. Accordingly, proteins displaying substantially equivalent or altered activity are likewise contemplated. These modifications may be deliberate, for example, such as modifications obtained through site-directed mutagenesis, or may be accidental, such as those obtained through mutations in hosts that are producers of the complex or its named subunits. Also, the
20 terms "elongation factor-2 kinase", "eEF-2 kinase", "EF-2 kinase", and "Cefk" are intended to include within their scope proteins specifically recited herein as well as all substantially homologous analogs and allelic variations.

- The amino acid residues described herein are preferred to be in the "L" isomeric form.
25 However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired fractional property of immunoglobulin-binding is retained by the polypeptide. NH₂ refers to the free amino group present at the amino terminus of a polypeptide. COOH refers to the free carboxy group present at the carboxy terminus of a polypeptide. In keeping with standard polypeptide nomenclature, *J. Biol. Chem.*,

243 3552-59 (1969). abbreviations for amino acid residues are shown in the following Table of Correspondence:

TABLE OF CORRESPONDENCE

5	<u>SYMBOL</u>	<u>AMINO ACID</u>	
	<u>1-Letter</u>	<u>3-Letter</u>	
	Y	Tyr	tyrosine
	G	Gly	glycine
	F	Phe	phenylalanine
10	M	Met	methionine
	A	Ala	alanine
	S	Ser	serine
	I	Ile	isoleucine
	L	Leu	leucine
15	T	Thr	threonine
	V	Val	valine
	P	Pro	proline
	K	Lys	lysine
	H	His	histidine
20	Q	Gln	glutamine
	E	Glu	glutamic acid
	W	Trp	tryptophan
	R	Arg	arginine
	D	Asp	aspartic acid
25	N	Asn	asparagine
	C	Cys	cysteine

It should be noted that all amino-acid residue sequences are represented herein by formulae whose left and right orientation is in the conventional direction of amino-terminus to carboxy-terminus. Furthermore, it should be noted that a dash at the

30

beginning or end of an amino acid residue sequence indicates a peptide bond to a further sequence of one or more amino-acid residues. The above Table is presented to correlate the three-letter and one-letter notations which may appear alternately herein.

- 5 A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*; *i.e.*, capable of replication under its own control.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA
10 segment may be attached so as to bring about the replication of the attached segment.

A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in its either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and
15 does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of
20 DNA (*i.e.*, the strand having a sequence homologous to the mRNA).

An "origin of replication" refers to those DNA sequences that participate in DNA synthesis.

- 25 A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences,
30 cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g.,

mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

5 Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, polyadenylation signals, terminators, and the like, that provide for the expression of a coding sequence in a host cell.

10 A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well
15 as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

20 An "expression control sequence" is a DNA sequence that controls and regulates the transcription and translation of another DNA sequence. A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then translated into the protein encoded by the coding sequence.

25

A "signal sequence" can be included before the coding sequence. This sequence encodes a signal peptide, N-terminal to the polypeptide, that communicates to the host cell to direct the polypeptide to the cell surface or secrete the polypeptide into the media, and this signal peptide is clipped off by the host cell before the protein leaves the cell. Signal

sequences can be found associated with a variety of proteins native to prokaryotes and eukaryotes.

The term "oligonucleotide," as used herein in referring to the probe of the present invention, is defined as a molecule comprised of two or more ribonucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and use of the method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides.

The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand

to hybridize therewith and thereby form the template for the synthesis of the extension product.

As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to
5 bacterial enzymes, each of which cut double-stranded DNA at or near a specific nucleotide sequence.

A cell has been "transformed" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. The transforming DNA may or may not be integrated
10 (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transforming DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in which the transforming DNA has become integrated into a chromosome so that it is inherited by daughter cells through chromosome
15 replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transforming DNA. A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

20

Two DNA sequences are "substantially homologous" when at least about 75% (preferably at least about 80%, and most preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard
25 software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., *supra*; DNA Cloning, Vols. I & II, *supra*; Nucleic Acid Hybridization, *supra*.

It should be appreciated that also within the scope of the present invention are DNA sequences encoding eIF-2 kinase which code for a protein having the same amino acid sequence as SEQ ID NO: 2, 4, and 10, but which are degenerate to SEQ ID NO: 1, 3, and 9. By "degenerate to" is meant that a different three-letter codon is used to specify a particular amino acid. It is well known in the art that the following codons can be used interchangeably to code for each specific amino acid:

	Phenylalanine (Phe or F)	UUU or UUC
	Leucine (Leu or L)	UUA or UUG or CUU or CUC or CUA or CUG
10	Isoleucine (Ile or I)	AUU or AUC or AUA
	Methionine (Met or M)	AUG
	Valine (Val or V)	GUU or GUC or GUA or GUG
	Serine (Ser or S)	UCU or UCC or UCA or UCG or AGU or AGC
	Proline (Pro or P)	CCU or CCC or CCA or CCG
15	Threonine (Thr or T)	ACU or ACC or ACA or ACG
	Alanine (Ala or A)	GCU or GCG or GCA or GCG
	Tyrosine (Tyr or Y)	UAU or UAC
	Histidine (His or H)	CAU or CAC
	Glutamine (Gln or Q)	CAA or CAG
20	Asparagine (Asn or N)	AAU or AAC
	Lysine (Lys or K)	AAA or AAG
	Aspartic Acid (Asp or D)	GAU or GAC
	Glutamic Acid (Glu or E)	GAA or GAG
	Cysteine (Cys or C)	UGU or UGC
25	Arginine (Arg or R)	CGU or CGC or CGA or CGG or AGA or AGG
	Glycine (Gly or G)	GGU or GGC or GGA or GGG
	Tryptophan (Trp or W)	UGG
	Termination codon	UAA (ochre) or UAG (amber) or UGA (opal)

It should be understood that the codons specified above are for RNA sequences. The corresponding codons for DNA have a T substituted for U.

Mutations can be made in SEQ ID NO: 1, 3, and 9 such that a particular codon is changed
5 to a codon which codes for a different amino acid. Such a mutation is generally made by making the fewest nucleotide changes possible. A substitution mutation of this sort can be made to change an amino acid in the resulting protein in a non-conservative manner (*i.e.*, by changing the codon from an amino acid belonging to a grouping of amino acids having a particular size or characteristic to an amino acid belonging to another grouping)
10 or in a conservative manner (*i.e.*, by changing the codon from an amino acid belonging to a grouping of amino acids having a particular size or characteristic to an amino acid belonging to the same grouping). Such a conservative change generally leads to less change in the structure and function of the resulting protein. A non-conservative change is more likely to alter the structure, activity or function of the resulting protein. The
15 present invention should be considered to include sequences containing conservative changes which do not significantly alter the activity or binding characteristics of the resulting protein.

The following is one example of various groupings of amino acids:

20

Amino acids with nonpolar R groups

Alanine

Valine

25 Leucine

Isoleucine

Proline

Phenylalanine

Tryptophan

30 Methionine

Amino acids with uncharged polar R groups

Glycine

Serine

5 Threonine

Cysteine

Tyrosine

Asparagine

Glutamine

10

Amino acids with charged polar R groups (negatively charged at pH 6.0)

Aspartic acid

Glutamic acid

15

Basic amino acids (positively charged at pH 6.0)

Lysine

Arginine

20 Histidine (at pH 6.0)

Another grouping may be those amino acids with phenyl groups:

Phenylalanine

25 Tryptophan

Tyrosine

Another grouping may be according to molecular weight (i.e., size of R groups):

30 Glycine

75

	Alanine	89
	Serine	105
	Proline	115
	Valine	117
5	Threonine	119
	Cysteine	121
	Leucine	131
	Isoleucine	131
	Asparagine	132
10	Aspartic acid	133
	Glutamine	146
	Lysine	146
	Glutamic acid	147
	Methionine	149
15	Histidine (at pH 6.0)	155
	Phenylalanine	165
	Arginine	174
	Tyrosine	181
	Tryptophan	204

20

Particularly preferred substitutions are:

- Lys for Arg and vice versa such that a positive charge may be maintained;
- Glu for Asp and vice versa such that a negative charge may be maintained;
- Ser for Thr such that a free -OH can be maintained; and
- 25 - Gln for Asn such that a free NH₂ can be maintained.

Amino acid substitutions may also be introduced to substitute an amino acid with a particularly preferable property. For example, a Cys may be introduced a potential site for disulfide bridges with another Cys. A His may be introduced as a particularly

30 "catalytic" site (*i.e.*, His can act as an acid or base and is the most common amino acid

in biochemical catalysis). Pro may be introduced because of its particularly planar structure, which induces β -turns in the protein's structure.

Two amino acid sequences are "substantially homologous" when at least about 70% of
5 the amino acid residues (preferably at least about 80%, and most preferably at least about 90 or 95%) are identical, or represent conservative substitutions.

A "heterologous" region of the DNA construct is an identifiable segment of DNA within a larger DNA molecule that is not found in association with the larger molecule in nature.
10 Thus, when the heterologous region encodes a mammalian gene, the gene will usually be flanked by DNA that does not flank the mammalian genomic DNA in the genome of the source organism. Another example of a heterologous coding sequence is a construct where the coding sequence itself is not found in nature (e.g., a cDNA where the genomic coding sequence contains introns, or synthetic sequences having codons different than
15 the native gene). Allelic variations or naturally-occurring mutational events do not give rise to a heterologous region of DNA as defined herein.

An "antibody" is any immunoglobulin, including antibodies and fragments thereof, that binds a specific epitope. The term encompasses polyclonal, monoclonal, and chimeric
20 antibodies, the last mentioned described in further detail in U.S. Patent Nos. 4,816,397 and 4,816,567.

An "antibody combining site" is that structural portion of an antibody molecule comprised of heavy and light chain variable and hypervariable regions that specifically
25 binds antigen.

The phrase "antibody molecule" in its various grammatical forms as used herein contemplates both an intact immunoglobulin molecule and an immunologically active portion of an immunoglobulin molecule.

30

Exemplary antibody molecules are intact immunoglobulin molecules, substantially intact immunoglobulin molecules and those portions of an immunoglobulin molecule that contains the paratope, including those portions known in the art as Fab, Fab', F(ab')₂ and F(v), which portions are preferred for use in the therapeutic methods described herein.

5

Fab and F(ab')₂ portions of antibody molecules are prepared by the proteolytic reaction of papain and pepsin, respectively, on substantially intact antibody molecules by methods that are well-known. See for example, U.S. Patent No. 4,342,566 to Theofilopolous et al. Fab' antibody molecule portions are also well-known and are produced from F(ab')₂ portions followed by reduction of the disulfide bonds linking the two heavy chain portions as with mercaptoethanol, and followed by alkylation of the resulting protein mercaptan with a reagent such as iodoacetamide. An antibody containing intact antibody molecules is preferred herein.

10

15 The phrase "monoclonal antibody" in its various grammatical forms refers to an antibody having only one species of antibody combining site capable of immunoreacting with a particular antigen. A monoclonal antibody thus typically displays a single binding affinity for any antigen with which it immunoreacts. A monoclonal antibody may therefore contain an antibody molecule having a plurality of antibody combining sites, each immunospecific for a different antigen; e.g., a bispecific (chimeric) monoclonal antibody.

20

The phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are physiologically tolerable and do not typically produce an allergic or similar untoward reaction, such as gastric upset, dizziness and the like, when administered to a human.

25

The phrase "therapeutically effective amount" is used herein to mean an amount sufficient to prevent, and preferably reduce by at least about 30 percent, more preferably by at least 50 percent, most preferably by at least 90 percent, a clinically significant

30

change in the S phase activity of a target cellular mass, or other feature of pathology such as for example, elevated blood pressure, fever or white cell count as may attend its presence and activity.

- 5 A DNA sequence is "operatively linked" to an expression control sequence when the expression control sequence controls and regulates the transcription and translation of that DNA sequence. The term "operatively linked" includes having an appropriate start signal (e.g., ATG) in front of the DNA sequence to be expressed and maintaining the correct reading frame to permit expression of the DNA sequence under the control of the
- 10 expression control sequence and production of the desired product encoded by the DNA sequence. If a gene that one desires to insert into a recombinant DNA molecule does not contain an appropriate start signal, such a start signal can be inserted in front of the gene.

- The term "standard hybridization conditions" refers to salt and temperature conditions
- 15 substantially equivalent to 5 x SSC and 65°C for both hybridization and wash. However, one skilled in the art will appreciate that such "standard hybridization conditions" are dependent on particular conditions including the concentration of sodium and magnesium in the buffer, nucleotide sequence length and concentration, percent mismatch, percent formamide, and the like. Also important in the determination of "standard hybridization
- 20 conditions" is whether the two sequences hybridizing are RNA-RNA, DNA-DNA or RNA-DNA. Such standard hybridization conditions are easily determined by one skilled in the art according to well known formulae, wherein hybridization is typically 10-20°C below the predicted or determined T_m with washes of higher stringency, if desired.

25

In one aspect, the present invention relates to the identification of a new superfamily of protein kinases centered around eEF-2 kinase. Accordingly, it includes the DNA sequences coding for these family members. In addition, the invention also contemplates that each member of this new protein kinase superfamily has its own cognate

phosphorylation target. As specified *supra*, two of these targets are eEF-2 and MHC, which are phosphorylated by eEF-2 kinase and MICK A, respectively.

In a particular embodiment, the present invention relates to phosphorylation target
5 analogs, which are short peptide sequences derived from phosphorylation targets of this new superfamily of protein kinases centered around eEF-2 kinase. Specifically, it is contemplated that these peptide analogs will be instrumental in the development of high throughput screening assays to identify inhibitors of members of this new superfamily.

10 As overexpression of eEF-2 kinase has been associated with a variety of cancers and other hyperproliferative pathologies (discussed *supra*), the invention also includes assay systems for the screening of potential drugs effective at inhibiting eEF-2 kinase activity. It is contemplated that any of the recited assays can be automated using technology that is standard to the skilled artisan.

15 As stated above, the present invention also relates to a recombinant DNA molecule or cloned gene, or a degenerate variant thereof, which encodes a eEF-2 kinase, or a fragment thereof, that possesses a molecular weight of about 100 kD and an amino acid sequence set forth in Figure 5 (SEQ ID NO: 2, 4, and 10); preferably a nucleic acid molecule, in
20 particular a recombinant DNA molecule or cloned gene, encoding the 100 kD eEF-2 kinase has a nucleotide sequence or is complementary to a DNA sequence shown in Figure 5 (SEQ ID NO: 1, 3, and 9).

Therapeutic possibilities are raised by the knowledge of the eEF-2 kinase sequence and
25 the existence of peptide analogs that can act as phosphorylation targets for the kinase. Accordingly, it is contemplated that sequences that are derived from the complement to the eEF-2 kinase mRNA sequence, and various modifications thereof, can act as potent antisense drugs that either inhibit expression in a competitive fashion, or, more effectively, by nuclease activity associated with the antisense drug that cleaves the eEF-2
30 kinase mRNA sequence, thus rendering it irreversibly inactive. Alternative therapeutics

are also contemplated that concern the use of peptides and peptide analogs representing portions of phosphorylation target amino acid sequences. It is envisioned that such peptide-based drugs would inhibit eEF-2 kinase activity on its native target, thus bypassing the cascade of events that would lead to malignant transformation.

5

The antisense or peptide-based drugs may be prepared in pharmaceutical compositions, with a suitable carrier and at a strength effective for administration by various means to a patient experiencing an adverse medical condition associated with specific malignancies for the treatment thereof. A variety of administrative techniques may be utilized, among
10 them parenteral techniques such as subcutaneous, intravenous and intraperitoneal injections, catheterizations and the like. Average quantities of the antisense or peptide-based drugs may vary and in particular should be based upon the recommendations and prescription of a qualified physician or veterinarian.

15 Also, antibodies including both polyclonal and monoclonal antibodies, and drugs that modulate the production or activity of eEF-2 kinase may possess certain diagnostic applications and may, for example, be utilized for the purpose of detecting and/or measuring levels of eEF-2 kinase. It is anticipated that further experimentation will reveal a prognostic correlation between eEF-2 kinase levels and the prediction and or
20 progression of certain malignancies associated with carcinoma. For example, eEF-2 kinase may be used to produce both polyclonal and monoclonal antibodies to themselves in a variety of cellular media, by known techniques such as the hybridoma technique utilizing, for example, fused mouse spleen lymphocytes and myeloma cells. Likewise, small molecules that mimic or antagonize the activity of eEF-2 kinase of the invention
25 may be discovered or synthesized, and may be used in diagnostic and/or therapeutic protocols.

The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal, antibody-producing cell lines can also be created by techniques other
30 than fusion, such as direct transformation of B lymphocytes with oncogenic DNA, or

transfection with Epstein-Barr virus. See, e.g., M. Schreier et al., "Hybridoma Techniques" (1980); Hammerling et al., "Monoclonal Antibodies And T-cell Hybridomas" (1981); Kennett et al., "Monoclonal Antibodies" (1980); see also U.S. Patent Nos. 4,341,761; 4,399,121; 4,427,783; 4,444,887; 4,451,570; 4,466,917;
5 4,472,500; 4,491,632; 4,493,890.

Panels of monoclonal antibodies produced against eEF-2 kinase peptides can be screened for various properties: *i.e.*, isotype, epitope, affinity, etc. Of particular interest are monoclonal antibodies that neutralize the activity of eEF-2 kinase. Such monoclonals
10 can be readily identified in eEF-2 kinase activity assays. High affinity antibodies are also useful when immunoaffinity purification of native or recombinant eEF-2 kinase is desired.

Preferably, the anti-eEF-2 kinase antibody used in the diagnostic methods of this
15 invention is an affinity purified polyclonal antibody. More preferably, the antibody is a monoclonal antibody (mAb). In addition, it is preferable for the anti-eEF-2 kinase antibody molecules used herein be in the form of Fab, Fab', F(ab')₂ or F(v) portions of whole antibody molecules.

20 As suggested earlier, the diagnostic method of the present invention comprises examining a cellular sample or medium by means of an assay including an effective amount of an antagonist to eEF-2 kinase, such as an anti-eEF-2 kinase antibody, preferably an affinity-purified polyclonal antibody, and more preferably a mAb. In addition, it is preferable for the anti-eEF-2 kinase antibody molecules used herein be in the form of Fab, Fab', F(ab')₂
25 or F(v) portions or whole antibody molecules. As previously discussed, patients capable of benefiting from this method include those suffering from cancer, a pre-cancerous lesion, a viral infection or other like pathological derangement. Methods for isolating the eEF-2 kinase and inducing anti-eEF-2 kinase antibodies and for determining and optimizing the ability of anti-eEF-2 kinase antibodies to assist in the examination of the
30 target cells are all well-known in the art.

Methods for producing polyclonal anti-polypeptide antibodies are well-known in the art. See U.S. Patent No. 4,493,795 to Nestor et al. A monoclonal antibody, typically containing Fab and/or F(ab')₂ portions of useful antibody molecules, can be prepared using the hybridoma technology described in *Antibodies - A Laboratory Manual*, Harlow and Lane, eds., Cold Spring Harbor Laboratory, New York (1988), which is incorporated herein by reference.

Splenocytes are typically fused with myeloma cells using polyethylene glycol (PEG) 6000. Fused hybrids are selected by their sensitivity to HAT. Hybridomas producing a monoclonal antibody useful in practicing this invention are identified by their ability to immunoreact with the present eEF-2 kinase and their ability to inhibit specified eEF-2 kinase activity in target cells.

A monoclonal antibody useful in practicing the present invention can be produced by initiating a monoclonal hybridoma culture comprising a nutrient medium containing a hybridoma that secretes antibody molecules of the appropriate antigen specificity. The culture is maintained under conditions and for a time period sufficient for the hybridoma to secrete the antibody molecules into the medium. The antibody-containing medium is then collected. The antibody molecules can then be further isolated by well-known techniques.

Media useful for the preparation of these compositions are both well-known in the art and commercially available and include synthetic culture media, inbred mice and the like. An exemplary synthetic medium is Dulbecco's minimal essential medium (DMEM; Dulbecco et al., *Virology* **8**:396 (1959)) supplemented with 4.5 gm/l glucose, 20mM glutamine, and 20% fetal calf serum. An exemplary inbred mouse strain is the Balb/c.

Methods for producing monoclonal anti-eEF-2 kinase antibodies are also well-known in the art. See Niman et al., *Proc. Natl. Acad. Sci. USA*, **80**:4949-4953 (1983). Typically, the present eEF-2 kinase or a peptide analog is used either alone or conjugated to an

immunogenic carrier, as the immunogen in the before described procedure for producing anti-eEF-2 kinase monoclonal antibodies. The hybridomas are screened for the ability to produce an antibody that immunoreacts with the eEF-2 kinase peptide analog and the present eEF-2 kinase.

5

The present invention further contemplates therapeutic compositions useful in practicing the therapeutic methods of this invention. A subject therapeutic composition includes, in admixture, a pharmaceutically acceptable excipient (carrier) and one or more of an anti-eEF-2 kinase antibody, peptide analog capable of competing for phosphorylation of
10 eEF-2 by eEF-2 kinase, antisense drug against eEF-2 kinase mRNA, or any other compound that is found to inhibit eEF-2 kinase activity. In a preferred embodiment, the composition comprises an antigen capable of modulating the activity of eEF-2 kinase within a target cell.

15 The preparation of therapeutic compositions which contain polypeptides, analogs or active fragments as active ingredients is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions, however, solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified. The active therapeutic
20 ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents which enhance the effectiveness of the active
25 ingredient.

A polypeptide, analog or active fragment can be formulated into the therapeutic composition as neutralized pharmaceutically acceptable salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the
30 polypeptide or antibody molecule) and which are formed with inorganic acids such as,

- for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed from the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine,
- 5 2-ethylamino ethanol, histidine, procaine, and the like.

The therapeutic polypeptide-, analog- or active fragment-containing compositions are conventionally administered intravenously, as by injection of a unit dose, for example. The term "unit dose" when used in reference to a therapeutic composition of the present

10 invention refers to physically discrete units suitable as unitary dosage for humans, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent: *i.e.*, carrier, or vehicle.

The compositions are administered in a manner compatible with the dosage formulation,

15 and in a therapeutically effective amount. The quantity to be administered depends on the subject to be treated, capacity of the subject's immune system to utilize the active ingredient, and degree of inhibition or neutralization of eEF-2 kinase activity desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are peculiar to each individual. However, suitable dosages may

20 range from about 0.1 to 20, preferably about 0.5 to about 10, and more preferably one to several, milligrams of active ingredient per kilogram body weight of individual per day and depend on the route of administration. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed by repeated doses at one or more hour intervals by a subsequent injection or other

25 administration. Alternatively, continuous intravenous infusion sufficient to maintain concentrations of ten nanomolar to ten micromolar in the blood are contemplated.

Formulations

30 Intravenous Formulation I

	<u>Ingredient</u>	<u>mg/ml</u>
	cefotaxime	250.0
	antibody, peptide, antisense drug, or other compound	10.0
	dextrose USP	45.0
5	sodium bisulfite USP	3.2
	edetate disodium USP	0.1
	water for injection q.s.a.d.	1.0 ml

Intravenous Formulation II

10	<u>Ingredient</u>	<u>mg/ml</u>
	ampicillin	250.0
	antibody, peptide, antisense drug, or other compound	10.0
	sodium bisulfite USP	3.2
	disodium edetate USP	0.1
15	water for injection q.s.a.d.	1.0 ml

Intravenous Formulation III

	<u>Ingredient</u>	<u>mg/ml</u>
	gentamicin (charged as sulfate)	40.0
20	antibody, peptide, antisense drug, or other compound	10.0
	sodium bisulfite USP	3.2
	disodium edetate USP	0.1
	water for injection q.s.a.d.	1.0 ml

25 Intravenous Formulation IV

	<u>Ingredient</u>	<u>mg/ml</u>
	antibody, peptide, antisense drug, or other compound	10.0
	dextrose USP	45.0
	sodium bisulfite USP	3.2
30	edetate disodium USP	0.1

water for injection q.s.a.d.

1.0 ml

As used herein, "pg" means picogram, "ng" means nanogram, "ug" or "μg" mean microgram, "mg" means milligram, "ul" or "μl" mean microliter, "ml" means milliliter.

5 "l" means liter.

Another feature of this invention is the expression of the DNA sequences disclosed herein. As is well known in the art, DNA sequences may be expressed by operatively linking them to an expression control sequence in an appropriate expression vector and
10 employing that expression vector to transform an appropriate unicellular host.

Such operative linking of a DNA sequence of this invention to an expression control sequence, of course, includes, if not already part of the DNA sequence, the provision of an initiation codon, ATG, in the correct reading frame upstream of the DNA sequence.

15

A wide variety of host/expression vector combinations may be employed in expressing the DNA sequences of this invention. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of SV40 and known bacterial plasmids, e.g., *E. coli*
20 plasmids col El, pCR1, pBR322, pMB9 and their derivatives, plasmids such as RP4; phage DNAs, e.g., the numerous derivatives of phage λ, e.g., NM989, and other phage DNA, e.g., M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2μ plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and
25 phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

Any of a wide variety of expression control sequences -- sequences that control the expression of a DNA sequence operatively linked to it -- may be used in these vectors to
30 express the DNA sequences of this invention. Such useful expression control sequences

include, for example, the early or late promoters of SV40, CMV, vaccinia, polyoma or adenovirus, the *lac* system, the *trp* system, the *TAC* system, the *TRC* system, the *LTR* system, the major operator and promoter regions of phage λ , the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the
5 promoters of acid phosphatase (e.g., Pho5), the promoters of the yeast α -mating factors, and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof.

A wide variety of unicellular host cells are also useful in expressing the DNA sequences
10 of this invention. These hosts may include well known eukaryotic and prokaryotic hosts, such as strains of *E. coli*, *Pseudomonas*, *Bacillus*, *Streptomyces*, fungi such as yeasts, and animal cells, such as CHO, RIL, B-W and L-M cells, African Green Monkey kidney cells (e.g., COS 1, COS 7, BSC1, BSC40, and BMT10), insect cells (e.g., Sf9), and human cells and plant cells in tissue culture.

15 It will be understood that not all vectors, expression control sequences and hosts will function equally well to express the DNA sequences of this invention. Neither will all hosts function equally well with the same expression system. However, one skilled in the art will be able to select the proper vectors, expression control sequences, and hosts
20 without undue experimentation to accomplish the desired expression without departing from the scope of this invention. For example, in selecting a vector, the host must be considered because the vector must function in it. The vector's copy number, the ability to control that copy number, and the expression of any other proteins encoded by the vector, such as antibiotic markers, will also be considered.

25 In selecting an expression control sequence, a variety of factors will normally be considered. These include, for example, the relative strength of the system, its controllability, and its compatibility with the particular DNA sequence or gene to be expressed, particularly as regards potential secondary structures. Suitable unicellular
30 hosts will be selected by consideration of, e.g., their compatibility with the chosen vector.

their secretion characteristics, their ability to fold proteins correctly, and their fermentation requirements, as well as the toxicity to the host of the product encoded by the DNA sequences to be expressed, and the ease of purification of the expression products.

5

Considering these and other factors, a person skilled in the art will be able to construct a variety of vector/expression control sequence/host combinations that will express the DNA sequences of this invention on fermentation or in large scale animal culture.

- 10 The present invention extends to the preparation of antisense oligonucleotides and ribozymes that may be used to interfere with the expression of the eEF-2 kinase gene at the translational level. This approach utilizes antisense nucleic acid and ribozymes to block translation of a specific mRNA, either by masking that mRNA with an antisense nucleic acid or cleaving it with a ribozyme.

15

- Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule. (See Weintraub, 1990; Marcus-Sekura, 1988.) In the cell, they hybridize to that mRNA, forming a double stranded molecule. The cell does not translate an mRNA in this double-stranded form. Therefore, antisense nucleic acids interfere with the expression of mRNA into protein. Oligomers of about fifteen nucleotides and molecules that hybridize to the AUG initiation codon will be particularly efficient, since they are easy to synthesize and are likely to pose fewer problems than larger molecules when introducing them into eEF-2 kinase-producing cells. Antisense methods have been used to inhibit the expression of many genes *in vitro* (Marcus-Sekura, 1988; Hambor et al., 1988).
- 20
- 25

- Ribozymes are RNA molecules possessing the ability to specifically cleave other single stranded RNA molecules in a manner somewhat analogous to DNA restriction endonucleases. Ribozymes were discovered from the observation that certain mRNAs have the ability to excise their own introns. By modifying the nucleotide sequence of
- 30

these RNAs, researchers have been able to engineer molecules that recognize specific nucleotide sequences in an RNA molecule and cleave it (Cech, 1988.). Because they are sequence-specific, only mRNAs with particular sequences are inactivated.

- 5 Investigators have identified two types of ribozymes, *Tetrahymena*-type and "hammerhead"-type. (Hasselhoff and Gerlach, 1988) *Tetrahymena*-type ribozymes recognize four-base sequences, while "hammerhead"-type recognize eleven- to eighteen-base sequences. The longer the recognition sequence, the more likely it is to occur exclusively in the target mRNA species. Therefore, hammerhead-type ribozymes
10 are preferable to *Tetrahymena*-type ribozymes for inactivating a specific mRNA species, and eighteen base recognition sequences are preferable to shorter recognition sequences.

The DNA sequences described herein may thus be used to prepare antisense molecules against, and ribozymes that cleave mRNAs for eEF-2 kinase .

15

- The present invention also relates to a variety of diagnostic applications, including methods for detecting and quantifying the levels of eEF-2 kinase. As mentioned earlier, eEF-2 kinase can be used to produce antibodies to itself by a variety of known techniques, and such antibodies could then be isolated and utilized as in tests for the
20 presence and levels of eEF-2 kinase activity in suspect target cells.

- As described in detail above, antibody(ies) to eEF-2 kinase can be produced and isolated by standard methods including the well known hybridoma techniques. For convenience, the antibody(ies) to eEF-2 kinase will be referred to herein as Ab₁ and antibody(ies)
25 raised in another species as Ab₂.

- The presence and levels of eEF-2 kinase in cells can be ascertained by the usual immunological procedures applicable to such determinations. A number of useful procedures are known. Three such procedures which are especially useful, utilize either
30 eEF-2 kinase labeled with a detectable label, antibody Ab₁ labeled with a detectable label,

or antibody Ab_2 labeled with a detectable label. The procedures may be summarized by the following equations wherein the asterisk indicates that the particle is labeled, and "~" stands for eEF-2 kinase:

- A. $\sim^* + Ab_1 = \sim^* Ab_1$
 5 B. $\sim + Ab^* = \sim Ab_1^*$
 C. $\sim + Ab_1 + Ab_2^* = \sim Ab_1 Ab_2^*$

The procedures and their application are all familiar to those skilled in the art and accordingly may be utilized within the scope of the present invention. The "competitive"
 10 procedure, Procedure A, is described in U.S. Patent Nos. 3,654,090 and 3,850,752. Procedure C, the "sandwich" procedure, is described in U.S. Patent Nos. RE 31,006 and 4,016,043. Still other procedures are known such as the "double antibody," or "DASP" procedure.

- 15 In each instance, eEF-2 kinase forms complexes with one or more antibody(ies) or binding partners and one member of the complex is labeled with a detectable label. The fact that a complex has formed and, if desired, the amount thereof, can be determined by known methods applicable to the detection of labels.
- 20 It will be seen from the above, that a characteristic property of Ab_2 is that it will react with Ab_1 . This is because Ab_1 raised in one mammalian species has been used in another species as an antigen to raise the antibody Ab_2 . For example, Ab_2 may be raised in goats using rabbit antibodies as antigens. Ab_2 therefore would be anti-rabbit antibody raised in goats. For purposes of this description and claims, Ab_1 will be referred to as a primary
 25 or anti-eEF-2 kinase antibody, and Ab_2 will be referred to as a secondary or anti- Ab_1 antibody.

The labels most commonly employed for these studies are radioactive elements, enzymes, chemicals which fluoresce when exposed to ultraviolet light, and others.

A number of fluorescent materials are known and can be utilized as labels. These include, for example, fluorescein, rhodamine, auramine, Texas Red, AMCA blue and Lucifer Yellow. A particular detecting material is anti-rabbit antibody prepared in goats and conjugated with fluorescein through an isothiocyanate.

5

eEF-2 kinase can also be labeled with a radioactive element or with an enzyme. The radioactive label can be detected by any of the currently available counting procedures. The preferred isotope may be selected from ^3H , ^{14}C , ^{32}P , ^{33}P , ^{35}S , ^{36}Cl , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{90}Y , ^{125}I , ^{131}I , and ^{186}Re .

10

Enzyme labels are likewise useful, and can be detected by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques. The enzyme is conjugated to the selected particle by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde and the like. Many enzymes which can be used in these procedures are known and can be utilized. The preferred are peroxidase, β -glucuronidase, β -D-glucosidase, β -D-galactosidase, urease, glucose oxidase plus peroxidase and alkaline phosphatase. U.S. Patent Nos. 3,654,090; 3,850,752; and 4,016,043 are referred to by way of example for their disclosure of alternate labeling material and methods.

20

A particular assay system developed and utilized in accordance with the present invention, is known as a receptor assay. In a receptor assay, the material to be assayed is appropriately labeled and then certain cellular test colonies are inoculated with a quantity of both the labeled and unlabeled material after which binding studies are conducted to determine the extent to which the labeled material binds to the cell receptors. In this way, differences in affinity between materials can be ascertained.

25

Accordingly, a purified quantity of the eEF-2 kinase may be radiolabeled and combined, for example, with antibodies or other inhibitors thereto, after which binding studies would be carried out. Solutions would then be prepared that contain various quantities

30

- of labeled and unlabeled uncombined eEF-2 kinase, and cell samples would then be inoculated and thereafter incubated. The resulting cell monolayers are then washed, solubilized and then counted in a gamma counter for a length of time sufficient to yield a standard error of <5%. These data are then subjected to Scatchard analysis after which
- 5 observations and conclusions regarding material activity can be drawn. While the foregoing is exemplary, it illustrates the manner in which a receptor assay may be performed and utilized, in the instance where the cellular binding ability of the assayed material may serve as a distinguishing characteristic.
- 10 In accordance with the above, an assay system for screening potential drugs effective to modulate the activity of eEF-2 kinase may be prepared. The eEF-2 kinase may be introduced into a test system, and the prospective drug may also be introduced into the resulting cell culture, and the culture thereafter examined to observe any changes in the eEF-2 kinase activity of the cells, due either to the addition of the prospective drug alone,
- 15 or due to the effect of added quantities of the known eEF-2 kinase. Alternatively, these assays can be carried out in a purely *in vitro* fashion as discussed below.

The following examples are presented in order to more fully illustrate the preferred embodiments of the invention. They should in no way be construed, however, as limiting

20 the broad scope of the invention.

EXPERIMENTAL DETAILS SECTION

EXAMPLE 1

- 25 **Peptide Sequencing.** eEF-2 kinase from rabbit reticulocyte lysate was purified as described (Hait et al., (1996) *FEBS Lett.* 397:55-60). Peptides were generated from the nitrocellulose-bound 103-kDa eEF-2 kinase protein by *in situ* tryptic digestion (Erdjument-Bromage et al., (1994) *Protein Sci.* 3:2435-2446) and fractionated by reverse-phase HPLC (Elicone et al., (1994) *J. Chromatogr.* 676:121-137) using a 1.0 mm Reliasil
- 30 C18 column. Selected peak fraction were then analyzed by a combination of automated

Edman sequencing and matrix-assisted laser-desorption time-of-flight mass spectrometry (Erdjument-Bromage et al., (1994)). The peptide sequences provided an essential lead into the cloning of eEF-2 kinase from human, mouse, rat, and *Caenorhabditis elegans*.

5

EXAMPLE 2

Molecular Cloning of cDNAs Encoding *C. elegans*, Mouse, Rat, and Human eEF-2 Kinases. To clone the cDNA for *C. elegans* eEF-2 kinase, oligonucleotide primers were designed based on the amino and carboxy termini of the predicted gene product from F42A10.4. Reverse transcriptase-PCR (RT-PCR) was performed using these primers and
10 total RNA from *C. elegans* (a gift from Monica Driscoll, Rutgers University). A single PCR product of ~2.3 kb was obtained and gel-purified using a gel extraction kit (Qiagen, Chatsworth, CA). The fragment was ligated into vector pCR2.1 using the TA cloning kit (Invitrogen, Sorrento Valley, CA), and then transformed into *Escherichia coli*. Plasmid DNA was purified, and restriction analysis used to verify the orientation of the coding
15 sequence with respect to the T7 promoter. Two clones (*Cefk-1* and *Cefk-2*, *C. elegans* eEF-2 kinase isoforms 1 and 2) were chosen and sequenced using a Li-Cor (Lincoln, NE) Long Read IR model 400L Automated DNA Sequencer. Analysis revealed that the two clones were identical except for a deletion of 24 bp in *Cefk-2* which corresponds to exon 4 and probably represents an alternatively spliced form.

20

To clone the mouse eEF-2 kinase, degenerate primers were designed based on the amino acid sequence of two peptides from rabbit eEF-2 kinase (LTPQAFSHFTFER (SEQ ID NO: 21) and LANXYYEKAE (SEQ ID NO: 22)): primer A, CA(G/A)GC(C/G/T/A)TT(C/T)(T/A)(C/G)(T/CCA(C/T)TT(C/T)AC(C/G/T/A)TT(C/
25 T)GA(G/A(C/A)G (SEQ ID NO: 23); and primer B, TC(C/G/T/A)GC(C/T)TT(C/T)TC(G/A)TA(G/A)TA(C/T)TT(G/A)TT(C/G/A/T)GC (SEQ ID NO: 24). RT-PCR was performed using primers A and B and poly(A)⁺ RNA from mouse spleen (CLONTECH). A single PCR product (~1.6 kb) was cloned into pCR2.1 (Invitrogen) and sequenced. Using sequence information from these mouse eEF-
30 2 kinase cDNA fragments, new primers were designed for 5' rapid amplification of

cDNA ends (RACE) and 3' RACE to obtain full-length mouse eEF-2 kinase cDNA. 5' RACE and 3' RACE were performed using Marathon-Ready mouse spleen cDNA (CLONTECH). This was carried out according to the manufacturer's instructions using the primers AP1 and C (TACAAATCAGCTGATGACCAGAACGCTC) (SEQ ID NO: 25) 5' antisense, or D (GGATTTGGACTGGACAAGAACCCCC) (SEQ ID NO: 19) 3' sense.

To clone rat eEF-2 kinases, PCR was performed on a rat PC12 cDNA library cloned in λ GT10 (CLONTECH) using primer B and vector primers. A 700-bp fragment was specifically amplified. The fragment was cloned into pCR2.1 (Invitrogen) and sequenced. This 700-bp fragments was radiolabeled and used to probe the same PC12 cDNA library (600,000 plaques). Fourteen positives were obtained in the initial screening. Five plaques were chosen for further analysis and sequencing based on insert sizes that ranged from 1.4 to 2.0 kb.

15

Recently, eEF-2 kinase from rabbit reticulocyte lysate was purified to near homogeneity (Hait et al., (1996)). This enabled determination of its partial amino acid sequence (see EXAMPLE 1). Two peptide sequences (LTPQAFSHFTFER and LANXYYEKAE) were compared with entries in a nonredundant database using the National Center for Biotechnology Information BLAST program (Altschul et al., (1990) *J. Mol. Biol.* 215:403-410). Matches were found with a *C. elegans* hypothetical protein (F42A10.4; GenBank accession number U10414). This sequence was obtained from the *C. elegans* genome sequencing project and is located on chromosome III (Wilson et al., (1994) *Nature* 368:32-38). The 100% identity between the sequenced peptides and the *C. elegans* protein, as well as the fact that the predicted molecular weight of the *C. elegans* protein is similar to that of eEF-2 kinase, suggested that this gene encoded eEF-2 kinase. The full-length cDNA by RT-PCR using *C. elegans* total RNA was cloned. Several clones were isolated and sequenced. *Cefk-1* has six of the predicted exons and encodes 768 amino acids. *Cefk-2* represents an alternatively spliced form that has five exons; it is missing amino acids 625-632 that correspond to exon four.

As is demonstrated in EXAMPLE 3, *C'efk-1* and *C'efk-2* have eEF-2 kinase activity when expressed in cell-free system using a wheat germ extract coupled transcription/translation system.

- 5 To determine the amino acid sequence of mammalian eEF-2 kinase, the cDNA of mouse eEF-2 kinase was cloned and sequenced. Since the sequenced peptides from rabbit eEF-2 were 100% identical to *C. elegans* eEF-2 kinase, then the two peptides should also match the sequence of mouse eEF-2 kinase. Degenerate primers were designed based on the amino acid sequence of the peptides and were used to perform
10 RT-PCR on mouse spleen poly(A)⁺ mRNA. A single PCR product of ~1.6 kb was obtained and sequenced. To obtain the full-length cDNA, 5' RACE and 3' RACE were performed using mouse spleen cDNA. The full-length cDNA, which encodes 724 amino acids, was expressed in a cell-free coupled transcription/translation system. A single translation product with an apparent molecular weight of 100 kDa was obtained
15 (Figure 2).

cDNA for rat eEF-2 kinase using a fragment of mouse eEF-2 kinase cDNA to probe a PC12 cDNA library was cloned and sequenced. However, after this work was completed, a paper describing the cloning of eEF-2 from rat skeletal muscle was
20 published (Redpath et al., (1996) *J. Biol. Chem.* 271:17547-17554) and the reported sequence appears to be identical to the eEF-2 kinase sequence from PC12 cells. Like the mouse eEF-2 kinase, the rat eEF-2 kinase cDNA encodes a 724-amino acid protein.

The human eEF-2 kinase cDNA was cloned and sequenced. RT-PCR was performed
25 on poly(A)⁺ mRNA from the human glioma cell line T98G using 20' mer primers corresponding to the 5' and 3' ends of the mouse eEF-2 kinase coding region. The human eEF-2 kinase cDNA encodes a 725 amino acid protein.

EXAMPLE 3

Expression of eEF-2 Kinase From *C. elegans*, Mouse, Rat, and Human in a Cell-Free System. Plasmid DNA from clones *Cefk-1*, *Cefk-2*, as well as mouse and human eEF-2 kinase cDNA were used in the TNT wheat germ extract coupled transcription/translation system (Promega). [³⁵S]Methionine-labeled products were then analyzed by SDS/PAGE. The reaction mixture (50 µl total volume) contained 1 µg of plasmid DNA and 26 µCi of [³⁵S]methionine (specific activity = 1175.0 Ci/mmol; 1 Ci = 37 GBq). Other components were added to the reaction mixture according to the manufacturer's protocol. The reaction mixture was incubated for 1.5 h at 30°C and terminated by incubation on ice. A 10 µl aliquot of the reaction mixture was mixed with 2 µl of 5X Laemmli buffer and boiled for 5 min. Samples were analyzed by SDS/PAGE on 8% gels and autoradiography.

The remainder of the transcription/translation reaction was diluted 4-fold with buffer A (20 mM Tris-HCl, pH 7.4/1 mM MgCl₂/10% glycerol/7 mM 2-mercaptoethanol) and applied to a HR5/5 Mono Q column (Pharmacia) equilibrated with buffer A. The column was developed with 20 column volumes of a 50-600 mM KCl linear gradient to buffer A.

To assay for eEF-2 kinase activity, 5 µl from each fraction was added to a reaction mixture (40 µl) containing 50 mM Hepes-KOH (pH 7.4) 10 mM magnesium acetate, 0.1 mM CaCl₂, 5 mM dithiothreitol, 50 µM ATP, 2 µCi [γ -³²P]ATP, 0.6 µg calmodulin, and 0.5 µg rabbit reticulocyte eEF-2. Reactions were incubated at 30°C for 2 min and were terminated by adding 20 µl of 3X Laemmli sample buffer. Samples were boiled for 5 min and proteins separated by SDS/PAGE on 8% gels. Phosphoproteins were analyzed by autoradiography.

To determine whether *Cefk-1* and *Cefk-2* have eEF-2 kinase activity, cell-free coupled transcription/translation system were expressed. Translation of *Cefk-1* and *Cefk-2* produced products with an apparent molecular weight of 100 kDa (Figure 2), which is

- slightly larger than the computer-predicted molecular weight of the protein but is identical to the molecular weight of a rabbit reticulocyte eEF-2 kinase as determined by SDS/PAGE. The translation products of the mixture of *Cefk-1* and *Cefk-2* are able to phosphorylate eEF-2 (Figure 3) and elute from a Mono Q column at the same position as endogenous *C. elegans* eEF-2 kinase (Figure 3A). The eEF-2 phosphorylation activity of the recombinant protein is Ca^{2+} /calmodulin-dependant (Figure 3C). The differences in the catalytic properties *Cefk-1* and *Cefk-2* isoforms are under current investigation.
- 10 Mouse and human eEF-2 kinase cDNAs were expressed in a coupled transcription/translation system and a product of ~100 kDa was obtained (Figure 2). As shown in Figure 3, the recombinant human eEF-2 kinase activity was strictly Ca^{2+} /calmodulin-dependant. The kinase activity was completely inhibited by the calmodulin antagonists trifluoperazine and *N*-(6-aminohexyl)-5-chloro-1-naphthalene-sulfonamide. Human eEF-2 kinase in bacteria as a glutathione S-transferase fusion protein was expressed and demonstrated that the ability of the recombinant enzyme to phosphorylate eEF-2 and to undergo autophosphorylation are strictly calmodulin-dependent.
- 15

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EXAMPLE 4

- Analysis of Mouse eEF-2 Kinase mRNA Expression in Various Tissues.** eEF-2 kinase and eEF-2 hybridizations were performed using a 1.6 kb *EcoRI* mouse cDNA fragment and a 2.6 kb *EcoRI* human cDNA fragment, respectively. cDNAs were labeled with [^{32}P]dCTP using the random-primed DNA labeling method (Feinberg and Vogelstein (1983) *Anal. Biochem.* 132:6-13). A multiple tissue Northern blot (CLONETECH) was prehybridized at 42°C for 16 h in a 50% formamide solution containing 10X Denhardt's, 5X SSPE, 2% SDS, and 100 µg/ml salmon sperm DNA. Hybridizations were completed in the same solution containing the ^{32}P -labeled probe (1 X 10⁶ cpm/ml; specific activity, ~1 X 10⁸ dpm/µg DNA) and 10% dextran sulfate at 42°C for 16 h. Blots were washed twice at room temperature (15 min) in 2X SSPE, 0.05%
- 25
- 30

SDS, and once at 50°C (15 min) in 0.5X SSPE, 0.5% SDS. RNA/cDNA hybrids were visualized by autoradiography.

5 Northern blot analysis shows that eEF-2 kinase is ubiquitously expressed in mouse tissues and is particularly abundant in skeletal muscle and heart (Figure 4). The abundance of eEF-2 kinase mRNA in muscle tissues may indicate that phosphorylation of eEF-2 is particularly important in muscle, or that there are additional substrates of eEF-2 kinase which are muscle-specific.

10

EXAMPLE 5

Lack of Homology of eEF-2 Kinase to Members of Eukaryotic Protein Kinase Superfamily. The alignment of the amino acid sequences of *C. elegans* and mammalian eEF-2 kinases is shown in Figure 5. Rat and mouse eEF-2 kinase are very
15 similar being 97% identical and differing by only 23 amino acids. Human eEF-2 kinase is 90% identical to mouse and rat eEF-2 kinase. In contrast, *C. elegans* eEF-2 kinase is found to be only 40% identical to mammalian eEF-2 kinase.

According to the current classification, eEF-2 kinase belongs to the family of closely
20 related calmodulin-dependent protein kinases. Surprisingly, upon analyzing eEF-2 kinase sequences, any homology to the other calmodulin-dependent kinases or to any other members of the protein kinase super-family was not found. The only motif which it shares with all other protein kinases is the GXGXXG motif (279-284 in *C. elegans* eEF-2 kinases; 295-300 in mouse eEF-2 kinase) which forms a glycine-rich loop and
25 is part of the ATP-binding site. Comparison of mammalian and *C. elegans* eEF-2 kinase revealed only one extended region of homology that spans ~200 amino acids upstream of the GXGXXG motif. The high degree of similarity and the proximity to the nucleotide-binding site suggests that these 200 amino acids represent the catalytic domain. This region has a high degree of similarity and a portion of this region (amino
30 acids 251-300 in mouse eEF-2 kinase) displays 75% identity to the catalytic domain of

MHCKA (see below), which also suggests that this is the catalytic domain. In the recently published rat eEF-2 kinase sequence [Redpath *et al.*, *J. Biol. Chem.* **271**: 17547-17554 (1996)], the catalytic domain was predicted to reside between amino acids 288 and 554 based on the homology with the catalytic domain of cAMP-dependant protein kinase (PKA). The results demonstrate that their prediction cannot be correct for several reasons. First, the homology of this region with PKA is not statistically significant. Second, this region is the least conserved between mammalian and *C. elegans* eEF-2 kinase. Finally, according to secondary structure predictions [made by Alexei V. Finkelstein, Institute of Protein Research, Russia using the ALB-GLOBULE program [Ptitsyn and Finkelstein, *Biopolymers* **22**:15-25 (1983)]], this region most likely has a distorted structure and contains almost no α -helices or β -strands, which are characteristic of a catalytic domain.

Because eEF-2 kinase is Ca^{2+} /calmodulin-dependant, it should contain a calmodulin-binding domain, which is usually represented by an amphipathic α -helix. There are several regions that could possibly assume an amphipathic α -helical conformation. Further biochemical analysis is required to determine which of these is the calmodulin-binding domain.

In the C-terminal region, there is a short stretch of 22 amino acids which is 86% identical between mammalian and *C. elegans* eEF-2 kinase and is preceded by a longer region of weak homology. One of the possibilities is that it is involved in oligomerization of the kinase. It was thought previously that eEF-2 kinase was an elongated monomer because it migrated during gel filtration as an ~150-kDa protein and migrated on SDS gels as a 105-kDa polypeptide [Ryazanov and Spirin, *Translational Regulation of Gene Expression*, Plenum, NY, Vol 2, pp 433-455 (1993); Abdelnajid *et al.*, *Int. J. Dev. Biol.*, **37**:279-290 (1993)]. However, the molecular weight of a monomer of mammalian eEF-2 kinase based on the predicted sequence is just 82 kDa. Thus, it is possible that eEF-2 kinase is not a monomer but a responsible for dimerization. Interestingly, according to computer prediction using the COIL

program, this conserved region can form a coiled-coil. Formation of coiled-coil is often responsible for dimerization [Lupas, *Trends Biochem. Sci.*, **21**:375-382 (1996)].

5

EXAMPLE 6

Striking Homology Between eEF-2 Kinase and MHCK A from *Dictyostelium*. It was found that eEF-2 kinases is homologous to the central portion of the recently described MHCKA from *Dictyostelium* [Futey *et al.*, *J. Biol. Chem.* **270**:523-529 (1995) see Figure 5]. The kinase was biochemically identified as a 130-kDa protein
10 and has a demonstrated role in myosin assembly, both *in vitro* and *in vivo* [Futey *et al.*, 1995, *supra*]. As with eEF-2 kinase, MHCKA displays no region with detectable similarity to the conserved catalytic domains found in known eukaryotic protein kinases. Primary structure analysis of MHCKA revealed an amino-terminal domain with a probable coiled-coil structure, a central nonrepetitive domain, and a C-terminal
15 domain consisting of seven WD repeats [Futey *et al.*, 1995, *supra*]. A fragment of the central nonrepetitive domain of MHCKA containing amino acids 552-841 was recently shown to represent the catalytic domain [Cote *et al.*, *J. Biol. Chem.* **272**:6846-6849 (1997)].

20 Because the catalytic domain of MHCKA and eEF-2 kinase have a high degree of similarity, the substrate specificity of these two kinases was assayed. Figure 6 shows that MHCK A cannot phosphorylate eEF-2, and likewise, rabbit eEF-2 kinase cannot use myosin heavy chains as a substrate. This demonstrated that each of these kinases is specific for their respective substrates.

25

EXAMPLE 7

eEF-2 Kinase and MHCK A Define a New Class of Protein Kinases. Members of the eukaryotic protein kinase superfamily are characterized by a conserved catalytic
30 domain containing approximately 260 amino acids and is divided into twelve

subdomains [Hanks and Hunter, *FASEB J.*, **9**:576-596 (1996); Hardie and Hanks, *The Protein Kinase Facts Book*, Academic, London (1995), Taylor *et al.*, *Annu. Rev. Cell Biol.*, **8**:429-462 (1992) Johnson *et al.*, *Cell*, **85**: 149-158 (1996)]. The three-dimensional structure of several protein kinases revealed that the catalytic domain

5 consists of two lobes. The smaller N-terminal lobe, which has a twisted β -sheet structure, represents the ATP-binding domain. The larger C-terminal lobe, which is predominantly α -helical is involved in substrate binding. At the primary structure level, the only motif similar between eEF-2 kinase, MHCK A, and other protein kinases is the GXGXXG motif which forms the loop interacting directly with the

10 phosphates of ATP [Hanks and Hunter, 1996, *supra*; Hardie and Hanks 1995, *supra*; Taylor *et al.*, *supra*]. In eukaryotic protein kinases, this motif is located at the very N terminus of the ATP-binding lobe of the catalytic domain. In contrast, in a eEF-2 kinase and MHCK A, this motif is close to the C terminus of the catalytic domain (see Figure 7). However, the overall topology of the ATP-binding subdomain of eEF-2

15 kinase and MHCK A can be similar to other protein kinases because the region upstream of the GXGXXG motif is strongly predicted to contain four or five β -strands and thus can form a twisted β -sheet.

However, the mechanism of ATP-binding to eEF-2 kinase is probably quite different

20 in comparison to other conventional members of the eukaryotic protein kinase superfamily. In protein kinases, there is a conserved lysine residue, corresponding to Lys-72 in cAMP-dependant protein kinases which binds to the β - and γ -phosphates of ATP and is located at about 20 amino acids downstream of the GXGXXG motif. Analysis of eEF-2 kinase and MHCK A sequences revealed that there are no conserved

25 lysine residues in the vicinity of the GXGXXG motif. There is another atypical protein kinase, BCR-ABLE, which does not contain this conserved lysine and it is proposed that it interacts with ATP *via* two cysteine residues [Maro and Witte, *Cell*, **67**:459-468 (1991)]. Interestingly, eEF-2 kinase and MHCK-A contain two conserved cysteine residues (Cys-313 and Cys-317 in mouse eEF-2 kinase) which are located near the

30 GXGXXG motif and therefore might be involved in ATP binding. Thus the

mechanism of ATP-binding of eEF-2 kinase and MHCK A is different from other members of the protein kinase superfamily, but may be similar to that of the BCR-ABLE protein kinase.

- 5 The overall catalytic mechanism of eEF-2 kinase and MHCKA is probably also very different from other eukaryotic protein kinases. All members of the eukaryotic protein kinase superfamily contain a DXXXN motif in the catalytic loop and a DFG motif in the activation segment [Hanks and Hunter, 1996; *supra*, Hardie and Hanks 1995, *supra*; Taylor *et al.*, *supra*; Johnson *et al.*, 1996, *supra*]. These two motifs, which are
10 directly involved in the catalysis of the protein phosphorylation reaction, are absent from the eEF-2 kinase and MHCK A catalytic domain.

- It is not known whether there are other protein kinases which are structurally similar to eEF-2 kinase and MHCK A. An extensive search of the entire nonrestricted
15 database of the National Center for Biotechnology Information using the BLAST program did not reveal any protein with a significant homology to the catalytic domain of eEF-2 kinase and MHCKA. A search of the Expressed Sequence Tag (EST) database revealed several ESTs from *C. elegans*, mouse and human which are essentially identical to portions of eEF-2 kinase cDNA sequences reported here.
20 Interestingly, a search of the recently completed genome database of *Saccharomyces cerevisiae* did not reveal any protein with homology to eEF-2 kinase despite the fact that eEF-2 phosphorylation was reported in yeast (41).

- Conclusion.** Since the catalytic domains of eEF-2 kinase and MHCK A do not share
25 homology with other known protein kinases, these two protein kinases establish the presence of a novel and widespread superfamily of eukaryotic protein kinases. Although the existence of several unusual protein kinases have been reported, to the knowledge, it was demonstrated for the first time the existence of a biochemically well-characterized and ubiquitous protein kinase that is structurally unrelated to other
30 serine/threonine/tyrosine kinases. Contrary to the widely accepted belief that all

eukaryotic protein kinases evolved from a single ancestor, the results suggest that eukaryotic protein kinases appeared at least twice during the course of evolution. This also suggests that, in addition to the relatively well-characterized catalytic mechanism employed by members of eukaryotic serine/threonine/tyrosine protein kinase
5 superfamily, there exists another mechanism of protein kinase superfamily, there exists another mechanism of protein phosphorylation. Further studies will reveal the molecular details of this mechanism and whether there are other protein kinases that phosphorylate their substrates using this mechanism.

10

EXAMPLE 8

Preparation of recombinant eEF-2 kinase fusion proteins with GST, 6xHis, and thioredoxin. Human eEF-2 kinase cDNA was cloned into three different expression vectors: pGEX-2T (Pharmacia Biotech, Piscataway, NJ); pRSET A (Invitrogen, Sorrento Valley, CA); and pThioHisB (Invitrogen). After transformation into *Escherichia coli*
15 strain BL21(DE3), transformants were cultured in LB broth containing 50 µg/ml ampicillin. When the culture reached an A_{600} value of 0.7, isopropyl-β-thiogalactopyranoside (IPTG) was added to the bacterial cultures to a final concentration of 0.5 µM to induce expression. After three hours, the cultures were harvested by centrifugation, and the cells were then sonicated. After extract preparation and analysis
20 by SDS-PAGE, it was found that all of the expressed tag forms of the eEF-2 kinase were in inclusion bodies. Inclusion bodies were precipitated, dissolved in 8.0 M urea, and dialyzed overnight against 20 mM Tris-HCl (pH 7.0) buffer containing 100 mM NaCl and 4 mM β-mercaptoethanol. The refolded protein was analyzed by SDS-PAGE and assayed for the ability to phosphorylate eEF-2. All of the fusion eEF-2 kinase
25 preparations were able to efficiently phosphorylate eEF-2.

EXAMPLE 9

eEF-2 Kinase Activity Assay Using a 16-Amino Acid Peptide Derived from Myosin Heavy Chain as the Phosphorylation Target. It was found that 16' mer peptide,
30 RKKFGESKTKTKIEFL, can serve as a good substrate for eEF-2 kinase. (Note: circular

dichroism measurements indicated that this peptide is in an α -helical structure, and that amidation of the peptide further stabilizes the α -helical structure, resulting in stronger phosphoacceptor activity.) Since recombinant eEF-2 is impossible to overexpress, as discussed *supra*, and large amounts of the protein are required to for large scale screening assays, the discovery of a peptide (easily synthesized on a large scale) that exhibits the same phosphoacceptor activity as eEF-2 was the critical breakthrough that allows for the development of a variety of automated high throughput screening assays for screening drug candidates.

10 The basic assay is as follows: 0.2-10.0 μ g of recombinant eEF-2 kinase (produced as described in EXAMPLE 6) is incubated with the 16' mer peptide (described above) in a buffer consisting of 12.5 mM Hepes-KOH (ph. 7.4), 2.5 mM magnesium acetate, 1.25 mM DTT, 25 μ M CaCl_2 , 0.05-2.5 μ g calmodulin, 100 μ M ATP, and 0.5 μ Ci [γ - ^{33}P]ATP in a total volume of 5-250 μ l. Samples are incubated at 30°C and aliquots can be withdrawn at various time points or at a single end point, and the reaction terminated by lowering the temperature ($\leq 4^\circ\text{C}$). The aliquots are then spotted onto phosphocellulose paper (2 cm x 2 cm) and washed (4 x 4 min) with 75 mM phosphoric acid. The papers are then rinsed with 100% ethanol, dried, and then counted in a scintillation counter. The assay can be performed at various peptide concentrations, as was done in the experiment illustrated in Figure 8. Clearly for a high throughput drug screening assay, that would be amenable to automation, the assays would most likely be performed using one peptide concentration with increasing amounts of different drug (inhibitor) candidates, and the data collected at a single time point. The assay can be performed in any one of the following formats:

- 25 1. with [γ - ^{32}P]ATP or [γ - ^{33}P]ATP and then detected using either standard scintillation counting, or detected in the format of a homogeneous assay using a Scintillation Proximity Assay, described in detail in both the Amersham Product Catalog (1997), pp. 252-258, and U.S. patent number 4,568,649;

2. in any of a number of standard immunoassay formats using antibodies that are specific for the phosphorylated form of the 16'mer peptide. Detection would then be, as described in more detail *supra*, through the use of either isotopically- or nonisotopically-labeled antibodies, secondary antibodies, or 16'mer peptide.

EXAMPLE 10

Cancer cell killing by chemotherapeutic drugs requires protein synthesis, and can be blocked by cycloheximide

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It has been well established that protein synthesis is required for apoptotic cell death induced by a variety of stimuli, including anticancer drugs. Inhibition of protein synthesis by cycloheximide prevent apoptotic cell death, and protects cancer cells from treatment with anticancer drugs. The exact molecular mechanism by which protein synthesis modulates cell death is unclear. The results demonstrated herein demonstrate that translational elongation factor-2 kinase (eEF-2 kinase) can be activated by a slight decrease in pH. Activation of this kinase leads to commonly observed during apoptotic cell death, activation of this kinase, and hence inhibition of protein synthesis during apoptosis, is expected to be anti-apoptotic. Because of the possible anti-apoptotic function of eEF-2 kinase, inhibition of eEF-2 kinase is expected to sensitize tumors to apoptotic cell death and anticancer drugs. Specifically, activation of eEF-2 kinase in hypoxic solid tumors (a low pH environment) is anti-apoptotic. Consequently, the specific inhibition of eEF-2 kinase can sensitize hypoxic solid tumors in apoptotic cell death and to the cytotoxic action of anticancer drugs.

25

One of the major obstacles in cancer therapy is the resistance of cancer cells to chemotherapeutic drugs. Of the many types of drug resistance, the most commonly addressed is multidrug resistance. Multidrug resistance is a particular phenotype which is characterized by an unusual resistance of cells to a variety of anticancer drugs with unrelated chemical structures. Among various mechanisms of multidrug resistance, the

30

most important and intensively studied is the multidrug resistance conferred by P-glycoprotein. According to the current model, P-glycoprotein protects cells by actively pumping drugs out of cells.

- 5 Recent evidence suggests that there is another type of drug resistance that involves inhibition of programmed cell death, or apoptosis. Due to intensive research in the past several years, it has become well established that anticancer drugs kill cells by inducing apoptosis. Apoptosis is an active process that is accompanied by activation of specific signal transduction pathways, and requires expression of specific proteins. Although
- 10 there are a few exceptions, in most cases, it has been observed that inhibition of protein synthesis by cycloheximide can block cell death induced by anticancer drugs. Table 1 provides a list of examples where it was demonstrated that cycloheximide can prevent cytotoxicity of anticancer drugs.
- 15 Table 1: Examples where cycloheximide was shown to protect cells and tissues from cell death caused by anticancer drugs.

Drug	Cell Type	Reference
Topoisomerase I inhibitors		
20 Camptothecin	HL-60 (human promyelocyte)	5. Gong et al. (1993) <i>J. Cell Physiol.</i> 157 :263-270.
Camptothecin	Mouse thymocytes	6. Onishi et al., (1993) <i>Biochem. Biophys. Acta</i> 1175 : 147-154.
CPT-11	PLC (human hepatoma)	7. Suzuki & Kato (1996) <i>Exp. Cell Res.</i> 227 :154-159.
Topoisomerase II inhibitors		
Doxorubicin (adriamycin)	V79 (rodent fibroblasts)	8. Bonner & Lawrence (1989) <i>Int. J. Radiat. Oncol. Biol. Phys.</i> 16 :1209-1212.

	Doxorubicin (adriamycin)	P388 (mouse leukemia); mice	9. Furusawa et al. (1995) <i>Biol. Pharm. Bull.</i> 18 :1367-1372.
	Doxorubicin (adriamycin)	murine intestinal tract; mouse thymocytes	10 Thakkar & Potten (1992) <i>Biochem. Pharm</i> 43 :1683-1691.
	Etoposide	Balb/C 3T3 (mouse fibroblasts); CCRF-CEM (human lymphoblast cells); L1012 (mouse leukemia cells)	11 Chow et al. (1988) <i>Biochem. Pharm</i> 37 :1117-1122.
	Etoposide	mouse thymocytes	12 Sun et al. (1994) <i>Biochem. Pharm.</i> 47 : 187-195.
5	Microtubule drugs		
	Taxol	KB (human epidermoid carcinoma);	13 Ling et al. (1998) <i>Int. J. Cancer</i> 75 :925-932
		A549 (human lung adenocarcinoma) MCF-7 (human breast)	14 Liebman et al. (1994) <i>Anticancer Drugs</i> 5 :287-292
	Vincristine	Ksu (human osteosarcoma)	15 Sakai et al. (1989) <i>Cancer Res.</i> 49 :1193-1196.
	Vincristine	CHO strain AA8	16 Kung et al. (1990) <i>Cancer Res.</i> 50 :7307-7317.
10	Colchicine	Ksu	15 Sakai et al. (1989) <i>Cancer Res.</i> 49 :1193-1196
	Other drugs		
	Ara-C	rat intestine	17. Verbin et al. (1973) <i>Cancer Res.</i> 33 :2086-2093.
	Nitrogen mustard	rat intestine	18 Lieberman et al. (1970) <i>Cancer Res.</i> 30 :942-951.
	5-AZT	mouse thymocytes	19 Kizaki et al. (1993) <i>Immunopharm.</i> 25 :19-27.

Cisplatin	CHO	20. Barry et al. (1990) <i>Biochem. Pharm.</i> 40 :2353-2362
Methotrexate	mice	21. Panasci et al. (1982) <i>Cancer Lett.</i> 15 :81-86.

- 5 While most of these studies were performed on cells in culture, there is also evidence that protein synthesis is required for the cytotoxic action of anticancer drugs *in vivo*. It was demonstrated by Furusawa et al. (9) that, in mice, the toxicity of doxorubicin as well as its antitumor effects, can be effectively counteracted by injection of cycloheximide. In another study (21) it was found that injection of cycloheximide can
- 10 significantly reduce the toxicity of methotrexate. Thus, inhibition of protein synthesis may be considered a mechanism that confers resistance to anticancer drugs.

Cellular mechanism of protein synthesis inhibition: elongation factor-2 phosphorylation: It appears that, although eEF-2 kinase is strictly Ca^{2+} /calmodulin-

15 dependant, it requires very low concentrations of Ca^{2+} /calmodulin for activity, and physiologically relevant changes of intracellular Ca^{2+} are unlikely to cause a strong effect on eEF-2 kinase activity. On the other hand, it appears that changes in pH can drastically modulate eEF-2 kinase (see Preliminary Results). At $\text{pH} \geq 7.4$, eEF-2 kinase activity is very low, and increased dramatically 10 to 20-fold upon a slight decrease in

20 pH to 6.6. Thus, eEF-2 kinase appears to be a proton-activated protein kinase. It was also found that the pH-dependance of eEF-2 kinase activity closely correlated with pH dependance of protein synthesis inhibition. This observation suggests that eEF-2 kinase may be responsible for protein synthesis inhibition during acidification of the cytoplasm. Since significant acidification occurs during apoptosis, this acidification

25 may result in the inhibition of protein synthesis due to activation of eEF-2 kinase and phosphorylation of eEF-2. Activation of eEF-2 kinase by acidic pH may explain the previously reported strong increase in eEF-2 phosphorylation seen in brain tissue from

Alzheimer's patients, as well as that seen in neurons after treatment with glutamate (35, 36).

The role of eEF-2 kinase in drug resistance: Activation of eEF-2 kinase by an acidic pH suggests that it may play an important role in regulation of protein synthesis during apoptosis. It is now well established that a significant decrease in intracellular pH is part of the apoptotic process. A drop in pH by 0.5-1 pH unit is universally observed during apoptosis induced by various agents, including anticancer drugs (37-43). It was found that at an intracellular pH of 6.5-6.8, eEF-2 becomes strongly phosphorylated. This phosphorylation of eEF-2 at an acidic pH may explain the inhibition of protein synthesis that was observed during apoptosis (44, 45).

Since apoptosis requires ongoing protein synthesis, phosphorylation of eEF-2, and the resulting inhibition of translation, may be an anti-apoptotic mechanism. Thus, it is suggested that eEF-2 phosphorylation is a cellular mechanism that can protect cells from apoptosis. To test this hypothesis, the effect of overexpression of eEF-2 kinase on drug resistance of mouse fibroblasts was tested. As is shown, overexpression of eEF-2 kinase increases approximately 10-fold the resistance of cells to different cytotoxic drugs, namely camptothecin and teniposide. This result suggests that eEF-2 kinase may be involved in modulation of drug resistance. Thus, inhibition of protein synthesis mediated by eEF-2 phosphorylation can protect cells from apoptotic cell death by various mechanisms that include up-and downregulation of expression of many genes. The pH-dependant increase in eEF-2 phosphorylation may also explain the previously observed dramatic increase in malignant cell resistance at low pH. It was demonstrated that at pH 6.5-6.8, different cell lines became more resistant to mitoxantrone, paclitaxel, and topotecan (46, 47).

Drug resistance related to activation of eEF-2 kinase can be particularly important in the hypoxic interior of solid tumors, which are characterized by acidic pH (48, 49). In fact, it was recently demonstrated that eEF-2 kinase activity is drastically

upregulated in tumor cell lines (161) and in invasive breast cancer specimens obtained from patients (162). Thus, eEF-2 kinase can be an important mechanism contributing to drug resistance of cancer cells.

5

Accordingly, specific inhibition of eEF-2 kinase can sensitize cancer cells to apoptotic cell death and to the cytotoxic action of anticancer drugs.

The results demonstrate that eEF-2 kinase was dramatically activated by a decrease in
10 pH within the range that occurs during apoptosis and that the pH-dependence of eEF-2 kinase activation correlated with protein synthesis inhibition *in vivo* and that overexpression of eEF-2 kinase in mouse fibroblasts increased their resistance to cytotoxic drugs. Using deletion mutagenesis, it was determined the tentative location of the various functional domains of eEF-2 kinase.

15

Activation of eEF-2 kinase by low pH: eEF-2 kinase is a Ca^{2+} /calmodulin-dependant enzyme whose only known substrate is eEF-2. Initially, it was suggested that the function of eEF-2 kinase was to phosphorylate eEF-2, and arrest protein synthesis in response to an elevation of Ca^{2+} levels in the cytoplasm. However, in a recent detailed
20 study of the relationship between intracellular Ca^{2+} levels, eEF-2 phosphorylation, and protein synthesis in GH3 cells, it was shown that a superphysiological increase in Ca^{2+} levels in the cytoplasm produced only an insignificant increase in eEF-2 phosphorylation that did not affect translation (34).

25 Analysis of the pH dependence of recombinant GST-eEF-2 kinase demonstrated that both autophosphorylation activity and eEF-2 phosphorylation activity were markedly pH-dependent. The pH-dependence of eEF-2 kinase activity was quantitatively analyzed using a synthetic 16mer peptide substrate (MH-1; RKKFGESKTKTKEFL-amide. MH-1 corresponds to the MICK A phosphorylation site in *Dictyostelium*
30 myosin heavy chains. It was found it to be an efficient substrate for eEF-2 kinase.

Activity of GST-eEF-2 kinase was assayed as follows: Purified GST-eEF-2 kinase was incubated with MH-1 (100 μ M final) in a buffer consisting of 25 mM Hepes-KOH (pH varying), 5 mM magnesium acetate, 2.5 mM DTT, 50 μ M CaCl_2 , 0.5 μ g calmodulin, 100 μ M ATP, and 0.5 μ Ci [γ - ^{33}P]-ATP (specific activity = 2000 Ci/mmol). The total
5 volume of the reaction was 50 μ l. The reaction was run at 30°C for various periods of time, and was terminated by incubation in an ice-water bath. An aliquot of each reaction was spotted onto a 2cm x 2 cm square of phosphocellulose paper and then washed 4 x 4 minutes in 75 mM phosphoric acid. After a 30 second rinse in 100% ethanol, the filter papers were dried, and then counted in a scintillation counter. To
10 assay for autophosphorylation activity, kinase assays were run as above except that the peptide was omitted from the reaction mixture.

Figure 10 shows that phosphorylation of the peptide is very ineffective at pH \geq 7.4, but when the pH drops to 6.6, eEF-2 kinase becomes dramatically activated. It was also
15 analyzed how calmodulin activates eEF-2 kinase at different pH. eEF-2 kinase assays were done as described above, but with different concentrations of calmodulin at pH 6.6 and at pH 7.4. It appears that at pH 6.6, the K_d for calmodulin is about 10^9 M, while at pH 7.4, the K_d is approximately 10^{-7} . These results suggest that changes in intracellular Ca^{2+} at physiological pH-will not significantly affect eEF-2 kinase activity,
20 which is consistent with recently reported results on GH3 cells (34).

To determine how specific this pH effect is for eEF-2 kinase, the pattern of protein phosphorylation at different pH in extracts from rat heart tissue was analyzed. A heart was dissected from a freshly killed rat and frozen in liquid nitrogen. The frozen tissue
25 was homogenized in a buffer containing 25 mM Hepes-KOH (pH 7.4), 100 mM NaCl, 3mM EDTA, 2mM EGTA, 40 μ g/ml soybean trypsin inhibitor, 0.5 mM PMSF, 20 mM Na pyrophosphate. The homogenate was clarified by centrifugation for 20 min. at 16,000 xg at 4°C. In order to assay for eEF-2 kinase activity, 10 μ l of the homogenate was added to a reaction mixture containing 50 mM Hepes-KOH (at various
30 pH), 10 mM magnesium acetate, 5 mM DTT, 100 μ M CaCl_2 , 0.5 μ g calmodulin, 60

μM ATP, and 2 μCi [$\gamma\text{-}^{33}\text{P}$]-ATP (specific activity = 2000 Ci/mmol). The total volume of the reaction was 40 μl . The reaction was run at 30°C for 5 minutes, and was terminated by incubation in an ice-water bath. Laemmli sample buffer was added, and the reaction mixture was boiled for 5 minutes. Samples were analyzed by 8% SDS-PAGE and autoradiography. As can be seen from Figure 3, eEF-2 was the only protein whose phosphorylation increased in response to a decrease in pH.

Next whether a decrease in pH_i of cells in culture resulted in inhibition of protein synthesis, and whether it correlated with activation of eEF-2 kinase were analyzed. Protein synthesis was measured in GH3 cells by [^3H]-Leu pulse-incorporation. GH3 cells were pre-incubated for 30 minutes in Ham's F-10 medium at 0.2 pH unit intervals from pH 6.0 to 8.0. Leucine pulse-incorporation was measured as described in Brostrom et al. (115). 1 mM Ca^{2+} and 100 μM [^3H]-Leu were added to the medium for a 15 minute incorporation period. Cells were harvested by centrifugation, washed, and lysed. Unincorporated label was removed by TCA precipitation, and Leu incorporation was measured by scintillation counting.

The actual intracellular pH was verified by incorporating BCECF/AM into GH3 cells in balanced salt solution buffered at pH 7.4 for 30 minutes. One set of cells was washed and re-suspended in normal balanced salt solutions at 0.2 pH unit intervals between 6.0 and 7.8. The other set of cells was re-suspended in high-K + buffer containing nigericin. A ratio of excitation of 485nm/440nm with emission at 530 nm was determined for each sample and pH_i was calculated as described by Thomas et al. (116).

The results of these experiments are shown in Figure 11. A decrease in the intracellular pH produced a strong inhibition of protein synthesis, which indeed correlated with the pH-dependence of eEF-2 kinase activity. These results demonstrate that eEF-2 phosphorylation may be a mechanism responsible for inhibiting protein synthesis at a low intracellular pH. Since the decrease in intracellular pH to the level

that strongly activates eEF-2 kinase is universally observed during apoptosis (37-43), this provides evidence that eEF-2 phosphorylation may be responsible for protein synthesis inhibition during apoptosis.

- 5 **Effect of overexpression of eEF-2 kinase on the cellular resistance to anticancer drugs:** Cell lines overexpressing eEF-2 kinase by stably transfecting NIH/3T3 cells with full length murine eEF-2 kinase cDNA were created. Murine eEF-2 kinase cDNA was cloned into pCMV-SPORT2 (GIBCO/BRL) under the control of a CMV promoter. NIH/3T3 cells were co-transfected with pCMV-SPORT2-EF2K and pSV2neo, using
10 Lipofectamine (GIBCO/BRL). Stable transformants were selected with G_{418} (0.5 mg/ml), and were further maintained in medium containing G_{418} . A control cell line (C13) was produced by co-transfection of NIH/3T3 cells with empty pCMV-SPORT2/pSV2neo. The expression of eEF-2 kinase mRNA in the selectants was assayed by Northern blot analysis. Two cloned cell lines, designated as E8 and E9
15 were found to overexpress significantly eEF-2 kinase mRNA, with E9 giving the maximal level of expression.

In order to verify that overexpression of eEF-2 kinase mRNA in E8 and E9 produced an increase in eEF-2 kinase activity, cell lysates were assayed for the ability to
20 phosphorylate eEF-2. eEF-2 kinase assays were performed as described above. E8 and E9 indeed showed greatly increased eEF-2 kinase activity in comparison to control cells. Overexpression of eEF-2 kinase did not have any effect on the growth parameters of cells. Cell cycle distribution of exponentially growing or quiescent cells, as well as growth rates, were the same for clones 8, 9 and control clones.

25

To answer the question whether eEF-2 kinase plays a role in resistance, clone E9 overexpressing eEF-2 kinase was incubated with two cytotoxic drugs, and assessed cell survival by MTT cytotoxicity assay. E9 and C13 were plated in 96-well plates at 3000 cells per well. Cells were grown in DMEM with 10% FCS for 1 day, and then
30 incubated with different concentrations of camptothecin (CPT) or teniposide (VM26)

for 4 days, and MTT assays were performed (Figure 12). E9 showed significantly increased resistance to these drugs.

EXAMPLE 11

5 **Expression and mutagenesis of recombinant human eEF2 kinase.**

Methods for efficient expression of recombinant eEF-2 kinase in bacteria, as well as generated and analyzed thirteen deletion mutants were developed. Expression of wild-type 6xHis-tagged and GST-tagged human eEF-2 kinase in *E. coli*. Initially, human eEF-
10 2 kinase was expressed as a fusion protein with 6xHis or glutathione-S-transferase (GST). Human eEF-2 kinase cDNA was cloned into two different expression vectors: pRSET (Invitrogen), and pGEX-2T (Pharmacia). After the resulting vectors were transformed into *E. coli* strain JM109(DE3), the transformants were cultured in LB broth containing 50 mg/ml ampicillin. At log phase growth, isopropyl-b-thiogalactopyranoside
15 (IPTG) was added to the bacterial cultures to a final concentration of 0.5 mM. After three hours, the cultures were harvested and the cells were sonicated.

Both 6xHis-tagged and GST-tagged eEF-2 kinase were efficiently expressed as judged by the appearance of one major band on Coomassie-stained gels after SDS-PAGE
20 analysis of crude lysates. Therefore, eEF-2 kinase activity was analyzed directly in the crude lysates. In order to assay for eEF-2 kinase activity, bacterial lysates were incubated with purified rabbit reticulocyte eEF-2 (0.5 mg) in a buffer consisting of 50 mM Hepes-KOH (pH 7.4), 10 mM magnesium acetate, 5 mM DTT, 100 mM CaCl₂, 0.5 mg calmodulin, 60 mM ATP, and 2 mCi [γ-³³P]-ATP (specific activity = 2000 Ci/mmol).
25 The total volume of the reaction was 40 ml. The reaction was run at 30°C for 10 minutes, and was terminated by incubation in an ice-water bath. Laemmli sample buffer was added, and the reaction mixture was boiled for 5 minutes. Samples were analyzed by 8% SDS-PAGE. The gel was dried and exposed to film overnight.

As can be seen in Figure 13, recombinant eEF-2 kinase expressed in *E. coli* undergoes autophosphorylation upon incubation with [γ - 32 P]-ATP and can efficiently phosphorylate eEF-2. The ability of eEF-2 kinase to undergo autophosphorylation was previously reported for the enzyme purified from rabbit reticulocyte lysate (139).

5 Autophosphorylated eEF-2 kinase was represented by two or three distinct bands, showing that autophosphorylation of eEF-2 kinase occurs at multiple sites, and slightly affects its mobility in the gel. Both the ability of eEF-2 kinase to autophosphorylate and phosphorylate eEF-2 were strictly calmodulin-dependent (see Figure 13).

- 10 **Localization of eEF-2 kinase functional domains by *in vitro* mutagenesis:** Using *in vitro* mutagenesis, thirteen mutants of eEF-2 kinase were obtained with deletions ranging from 36 to 76 amino acids that systematically span the entire

eEF-2 kinase molecule: *In vitro* mutagenesis was done with the Muta-Gene Phagemid

15 *In Vitro* Mutagenesis kit from Bio-Rad which is based on a method developed by Kunkel (117). Human eEF-2 kinase cDNA was cloned into pCR2.1 (Invitrogen). This plasmid has an f1 ori so that it can exist as single-stranded, as well as double-stranded DNA. It also carries the genes for ampicillin and kanamycin resistance. Thus, this plasmid was found to be suitable for use with the Muta-Gene kit

20

The construct was transformed into *E. coli* strain CJ236, a *dut ung* strain. The enzymes dUTPase and uracil-N-glycosylase have been mutated and are non-functional, thus allowing for a large pool of uracil to be maintained in the cell as well as to allow uracil to be incorporated into the replicated plasmid. Bacteria carrying the plasmid were

25 selected by growth in medium containing ampicillin. In order to produce single-stranded DNA, cultures of CJ236 were infected with helper phage M13K07. Replication of the M13K07 genome has been partly disabled and, thus, the low copy number of the M13K07 genome allows for more packaging of the plasmid instead of helper phage. This minimizes contamination of the harvested single-stranded DNA with M13K07 DNA.

30 There is a kanamycin resistance marker in the M13K07 genome which allows for

selection of infected bacteria by growing them in the presence of kanamycin. After purification from the helper phage, the single-stranded DNA was mutagenized. 30-mer oligonucleotides were synthesized which were complementary to a stretch of fifteen nucleotides on each side of the region to be deleted. Annealing of the oligo to single-
5 stranded DNA caused the region to be deleted to loop out. The oligo acted as a primer for second- strand synthesis by T7 DNA polymerase. Synthesis was done in the presence of thymidine so that the resulting double-stranded construct was a hybrid of a uracil-containing strand and a thymidine-containing strand. The mutant plasmid was then transformed into *E. coli* strain DH5a. This strain has a functional uracil-N-glycosylase
10 which inactivates the uracil-containing strand and allows the thymidine-containing strand to be replicated. After purification, the mutant plasmid was sequenced to verify that the proper deletion was made. Initially, the resulting thirteen mutants were expressed *in vitro* in a coupled transcription/translation system and assayed for eEF-2 kinase activity.

15 Although using an *in vitro* transcription/translation system is fast and efficient, there are two disadvantages. First, it is not quantitative. Second, the amount of protein expressed *in vitro* is very low. To overcome this problem, the thirteen mutants were cloned into pGEX-2T (Pharmacia), and expressed as GST fusion proteins in *E. coli*.

20 Expression of GST-eEF-2 kinase deletion mutants in bacteria and purification. All thirteen mutants were expressed in *E. coli* BL21(DE3) as GST-tagged proteins. Expression of GST-tagged human eEF-2 kinase was done as follows: the cDNA for the mutant forms human eEF-2 kinase was cloned into pGEX-2T, and transformed into *E. coli* BL21(DE3). Cultures were grown at 37°C, and at log phase growth, protein
25 expression was induced with IPTG added to a final concentration of 0.5 mM. After a 3 hour incubation at 37°C with IPTG, cells were harvested by centrifugation.

Since wild-type and mutant eEF-2 kinase were found to be highly insoluble, the proteins were purified from inclusion bodies. Bacterial cells were re-suspended in sonication
30 buffer (phosphate-buffered saline, 1 mg/ml lysozyme, 3 mM EDTA, 40 mg/ml soybean

trypsin inhibitor, 0.5 mM PMSF, 20 mM Na pyrophosphate) and sonicated. Lysate was centrifuged at 16,000xg for 30 minutes at 4°C to pellet inclusion bodies. Pellet was re-suspended in a buffer containing 20 mM Tris-HCl (pH 7.0), 100 mM NaCl, 7 mM b-mercaptoethanol, 6 M urea and incubated on ice for 20 minutes. Lysate was dialyzed
5 overnight at 4°C against buffer consisting of 20 mM Tris-HCl (pH 7.0), 100 mM NaCl, and 7 mM b-mercaptoethanol. Dialyzed material was centrifuged at 16,000 xg for 20 min. at 4°C to remove any remaining insoluble material.

Glutathione-agarose (Sigma) was added to the dialysate (bed volume = 1/2000 of culture
10 volume), and incubated at 4°C for 2 hours with gentle shaking. Glutathione agarose was pelleted by centrifugation and washed 3x with PBS (10x bed volume). Bound GST-EF-2 kinase was eluted with 50 mM Tris-HCl (pH 8.0) containing 25 mM reduced glutathione (Volume of elution buffer = bed volume). Elution was done on ice for 20 minutes.

15 **Analysis of activity of deletion mutants:** The thirteen deletion mutants were assayed for the ability to phosphorylate eEF-2 and to undergo autophosphorylation. eEF-2 (Figure 14) kinase assays were performed as described above using purified rabbit reticulocyte eEF-2 as a substrate, and the pH of the reaction was 6.4. Mutants with deletions between amino acids 51-335 were neither able to phosphorylate eEF-2 nor to
20 undergo autophosphorylation. On the other hand, deletions between amino acids 521-725 caused a loss of eEF-2 kinase activity, but not a loss of autophosphorylation activity. This demonstrates that the catalytic domain is located between amino acids 51-335 while the region between amino acids 521-725 is important for eEF-2 recognition. The region between amino acids 336-520 probably serves as a hinge between two domains.

25

A summary of the results of mutational analysis of human eEF-2 kinase is shown in Figure 14. Mutational analysis reveals that eEF-2 kinase can be subdivided into two domains connected by a hinge region. The N-terminal domain represents the catalytic domain, and the C-terminal domain represents the eEF-2 targeting domain. This is
30 consistent with the location of the catalytic domain as predicted by comparison of eEF-2

kinases from different species (27). As was discussed in the Background and Significance section, the amino acid sequence of this region displays no homology to the catalytic domains of the conventional protein kinases, but appears to be highly similar to the catalytic domains of the recently described myosin heavy chain kinases from
5 *Dictyostelium*. Further experiments will define more precisely the location of the functional domains.

The results clearly demonstrate that the location of the catalytic domain of rat eEF-2 kinase suggested by Redpath *et al.* (140) in between amino acids 288-554 is incorrect.
10

Location of calmodulin-binding domain: In all mutants able to undergo autophosphorylation, this phosphorylation was strictly calcium/ calmodulin-dependent, suggesting that the calmodulin-binding region is located within amino acids 51 to 335.
15 To locate the calmodulin-binding domain more precisely, five mutants were analyzed with deletions between amino acids 51 to 355 for their ability to bind calmodulin-agarose. The only mutant of eEF-2 kinase not able to bind calmodulin-agarose contains a deletion of amino acids 51-96. The actual calmodulin-binding site is probably within amino acids 81 to 94 (FKEAWKHAIQKAKH), which are predicted to form an
20 amphipathic α -helix. The homologous sequence from *C. elegans* eEF-2 kinase (LMETWRKAARRART) is also predicted to form an amphipathic α -helix.

Expression of correctly-folded eEF-2 kinase: Although GST- and 6xHis-eEF-2 kinase expressed in bacteria was enzymatically active, the majority of recombinant protein
25 ended up in inclusion bodies. The inclusion bodies were precipitated, dissolved in 8M urea, and dialyzed overnight against 20 mM Tris buffer (pH 7.0) containing 100 mM NaCl and 4 mM b-mercaptoethanol. The refolded protein was analyzed by SDS-PAGE and assayed for the ability to undergo autophosphorylation and to phosphorylate eEF-2. Preparations of refolded GST-eEF-2 kinase and 6xHis-eEF-2 kinase contained
30 predominantly one band corresponding to eEF-2 kinase. In the case of GST-tagged eEF-

2 kinase, the protein was further purified using glutathione-Sepharose. Gel filtration analysis of recombinant eEF-2 kinase on Superdex-200 revealed that both 6xHis- and GST-eEF-2 kinase eluted predominantly in the void volume, indicating that it was aggregated. This aggregated kinase was enzymatically inactive. eEF-2 kinase activity
5 eluted in the fractions corresponding to a Stokes radius of 52. Approximately 4% of the refolded eEF-2 kinase eluted in this area. The specific activity of eEF-2 kinase was 5 mmoles/min/mg, which is slightly higher than the specific activity of eEF-2 kinase purified from rabbit reticulocytes. The extremely low yield of active eEF-2 kinase prompted to search for alternative methods for expression of recombinant kinase.

10

eEF-2 kinase was expressed as fusion with thioredoxin in order to obtain a soluble protein because it was reported that thioredoxin can prevent accumulation of recombinant proteins in inclusion bodies (149). Human eEF-2 kinase cDNA was cloned into the expression vector pThioHis (Invitrogen). The thioredoxin expressed from this vector has
15 additional histidine residues so it can also function as a His tag. Thioredoxin-eEF-2 kinase was found to remain soluble and was enzymatically active. Moreover, its elution profile on Mono Q and Superdex-200 was very similar to eEF-2 kinase purified from rabbit reticulocytes, which shows that it was correctly folded. This His-thioredoxin-tagged kinase can be efficiently and easily purified from total lysates by immobilized
20 metal affinity chromatography (IMAC) or by ThioBond resin (Invitrogen). This fusion protein also contains an enterokinase cleavage site, which allows for removal of the His-thioredoxin tag. Thus, a method to express active and, most likely correctly folded, eEF-2 kinase which will facilitate the studies was demonstrated.

25 **Phosphorylation of synthetic peptides by eEF-2 kinase:** Redpath *et al.* (118) were able to detect some [γ - 32 P]-ATP incorporation into a synthetic peptide corresponding to residues 49-60 of eEF-2 (RAGETRFTDTRK), which encompasses the phosphorylation site of eEF-2. The rate of phosphorylation was low, and the K_m was very high (>2.5 mM). A larger peptide corresponding to amino acids 48-66 of eEF-2

(ARAGETRFTDTRKDEQERC). was synthesized and was unable to detect any phosphorylation after incubation with [γ - 32 P]-ATP and recombinant eEF-2 kinase.

As can be seen in Figure 15, eEF-2 kinase can efficiently phosphorylate MH-1. The K_m of this reaction was approximately 150 mM, which is similar to the K_m of the phosphorylation of MH-1 by MHCK A (105 mM; 119). If an α -helical conformation is necessary for recognition of MH-1 by eEF-2 kinase, then removal of the C-terminal amide from MH-1 should reduce the α -helical propensity of the peptide, and thus, make it a less efficient substrate for eEF-2 kinase. As can be seen in Figure 11a, this is the case. An uncapped version of the peptide (called MH-U) can serve as a substrate for eEF-2 kinase, although a significantly less efficient one. The reduction of phosphorylation efficiency is due entirely to a change in K_m , which for MH-U is approximately 400 mM.

It is interesting that the sequence of MH-1 is quite different from the sequence surrounding the phosphorylation site in eEF-2 (see Figure 15B). When looking at the primary structure, the threonines that undergo phosphorylation are surrounded in these two peptides by very different amino acids. But when the same sequences are folded into α -helices, the surrounding environment of those phosphoacceptor threonines is very similar, as can be seen in Figure 15B: in both cases, there is a basic amino acid to the left and a glutamate followed by a basic amino acid on the right. This pattern may represent the consensus sequence for recognition by eEF-2 kinase and the related protein kinases. Thus, as demonstrated herein eEF-2 kinase phosphorylates amino acids located within α -helices.

25

While the invention has been described and illustrated herein by references to various specific material, procedures and examples, it is understood that the invention is not restricted to the particular material combinations of material, and procedures selected for that purpose. Numerous variations of such details can be implied as will be appreciated by those skilled in the art.

30

WHAT IS CLAIMED IS:

- 1 1. A protein kinase which is a member of a superfamily, said protein kinase
2 being characterized by:
 - 3 A. greater than 40% sequence similarity with eEF-2 kinase from
4 any organism; and,
 - 5 B. phosphorylates an amino acid within an alpha helical domain
6 of its target protein.
- 1 2. A protein kinase of Claim 1 which phosphorylates eukaryotic elongation
2 factor-2 (eEF-2), and is designated as eukaryotic elongation factor-2 kinase (eEF-2
3 kinase).
- 1 3. A protein kinase of Claim 1 which phosphorylates eukaryotic myosin heavy
2 chain (MHC), and is designated as myosin heavy chain kinase (MHCK).
- 1 4. A protein kinase of Claim 1 that phosphorylates a peptide sequence derived
2 from the phosphorylation site of a target protein.
- 1 5. A peptide sequence having SEQ ID NO: 20.
- 1 6. A protein kinase of Claim 1 which is a polypeptide having an amino acid
2 sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, and
3 SEQ ID NO: 10, and fragments thereof.
- 1 7. A protein kinase of Claim 1 which is derived from mammalian cells.
- 1 8. A protein kinase of Claim 1 labeled with a detectable label.

- 1 9. A protein kinase of Claim 8 wherein the label is selected from enzymes,
2 chemicals which fluoresce, and radioactive elements.
- 1 10. An antibody to the protein kinase of Claim 1.
- 1 11. An antibody to the phosphorylated form of the target protein of Claim 1.
12. An antibody to the phosphorylated form of the peptide of Claim 5.
- 1 13. The antibody of Claim 10, 11 or 12 which is a polyclonal antibody.
- 1 14. The antibody of Claim 10, 11 or 12 which is a monoclonal antibody.
- 1 15. An immortal cell line that produces a monoclonal antibody according to
2 Claim 14.
- 1 16. The antibody of Claim 10, 11 or 12 labeled with a detectable label.
- 1 17. The antibody of Claim 10, 11 or 12 wherein the label is selected from
2 enzymes, chemicals which fluoresce and radioactive elements.
- 1 18. A DNA sequence which encodes eEF-2 kinase, or a fragment thereof,
2 selected from the group consisting of:
3 (A) the DNA sequences of Figure 5 (SEQ ID NO: 1);
4 (B) the DNA sequences of Figure 5 (SEQ ID NO: 3);
5 (C) the DNA sequences of Figure 5 (SEQ ID NO: 9);
6 (D) DNA sequences that hybridize to any of the foregoing DNA
7 sequences under standard hybridization conditions;
8 (E) DNA sequences that code for expression of an amino acid sequence
9 encoded by any of the foregoing DNA sequences.

- 10 (F) degenerate variants thereof;
- 11 (G) alleles thereof; and,
- 12 (H) hybridizable fragments thereof.

1 19. A recombinant DNA molecule comprising a DNA sequence which encodes
2 eEF-2 kinase, or a fragment thereof, selected from the group consisting of:

- 3 (A) the DNA sequences of Figure 5 (SEQ ID NO: 1);
- 4 (B) the DNA sequences of Figure 5 (SEQ ID NO: 3);
- 5 (C) the DNA sequences of Figure 5 (SEQ ID NO: 9);
- 6 (D) DNA sequences that hybridize to any of the foregoing DNA
7 sequences under standard hybridization conditions;
- 8 (E) DNA sequences that code for expression of an amino acid sequence
9 encoded by any of the foregoing DNA sequences.
- 10 (F) degenerate variants thereof;
- 11 (G) alleles thereof; and,
- 12 (H) hybridizable fragments thereof.

1 20. The recombinant DNA molecule of either of Claims 18 or 19, wherein said
2 DNA sequence is operatively linked to an expression control sequence.

1 21. The recombinant DNA molecule of Claim 20, wherein said expression
2 control sequence is selected from the group consisting of the early or late promoters
3 of SV40 or adenovirus, the *lac* system, the *trp* system, the *TAC* system, the *TRC*
4 system, the major operator and promoter regions of phage λ , the control regions of
5 fd coat protein, the promoter for 3-phosphoglycerate kinase, the promoters of acid
6 phosphatase and the promoters of the yeast α -mating factors.

1 22. A probe capable of screening for eEF-2 kinase in alternate species prepared
2 from the DNA sequence of Claim 18.

1 23. A probe capable of screening for members of the protein kinase superfamily
2 of Claim 1 prepared from the DNA sequence of Claim 18.

1 24. A unicellular host transformed with a recombinant DNA molecule
2 comprising a DNA sequence or degenerate variant thereof, which encodes a protein
3 kinase, or a fragment thereof, selected from the group consisting of:
4 (A) the DNA sequences of Figure 5 (SEQ ID NO: 1);
5 (B) the DNA sequences of Figure 5 (SEQ ID NO: 3);
6 (C) the DNA sequences of Figure 5 (SEQ ID NO: 9);
7 (D) DNA sequences that hybridize to any of the foregoing DNA
8 sequences under standard hybridization conditions; and
9 (E) DNA sequences that code on expression for an amino acid sequence
10 encoded by any of the foregoing DNA sequences;
11 wherein said DNA sequence is operatively linked to an expression control
12 sequence.

1 25. The unicellular host of Claim 24 wherein the unicellular host is selected from
2 the group consisting of *E. coli*, *Pseudomonas*, *Bacillus*, *Streptomyces*, yeasts, CHO,
3 R1.1, B-W, L-M, COS 1, COS 7, BSC1, BSC40, and BMT10 cells, plant cells,
4 insect cells, and human cells in tissue culture.

1 26. A method for detecting eEF-2 kinase and assessing eEF-2 kinase levels by:
2 A. contacting a biological sample from a mammal in which the
3 presence or activity of said eEF-2 kinase is suspected with a binding partner of said
4 eEF-2 kinase under conditions that allow binding of said eEF-2 kinase to said
5 binding partner to occur; and,
6 B. detecting whether binding has occurred, and to what degree,
7 between said eEF-2 kinase from said sample and the binding partner;

8 wherein the detection of binding indicates that presence or activity of said
9 eEF-2 kinase in said sample, and indicates a level of said eEF-2 kinase in the
10 sample.

1 27. An assay system for screening drugs and other agents for ability to modulate
2 eEF-2 kinase activity, comprising a predetermined amount of eEF-2 kinase mixed
3 with varying amounts of drug or agent, along with target protein and ATP; wherein
4 detection is *via* either a detectable label on the γ -phosphate of ATP, or on an
5 antibody directed against the phosphorylated target protein..

1 28. The assay system of Claim 27 wherein the label on the γ -phosphate of ATP
2 comprises one of the following:

- 3 A. ^{32}P ;
- 4 B. ^{33}P
- 5 C. ^{35}S
- 6 D. a biotinylated phosphate moiety; or,
- 7 E. a fluorescent phosphate moiety.

1 29. The assay system of Claim 27 wherein the label on the antibody comprises
2 one of the following:

- 3 A. an enzyme detectable with colorimetric, fluorescent, or
4 chemiluminescent substrates, such as alkaline phosphatase or horseradish
5 peroxidase;
- 6 B. a biotin moiety;
- 7 C. a fluorescent moiety; or,
- 8 D. a radioactive moiety chosen from the following group of
9 isotopes: ^3H , ^{14}C , ^{32}P , ^{33}P , ^{35}S , ^{36}Cl , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{90}Y , ^{125}I , ^{131}I , and ^{186}Re .

1 30. An assay system for screening drugs and other agents for ability to modulate
2 eEF-2 kinase activity, comprising:

- 3 A. culturing an observable cellular test colony inoculated with a
4 drug or agent;
5 B. harvesting a supernatant from said cellular test colony; and,
6 C. examining said supernatant for the presence of said eEF-2
7 kinase activity wherein an increase or a decrease in a level of said eEF-2 kinase
8 activity indicates the ability of a drug to modulate the activity of said eEF-2 kinase.

1 31. A test kit for assessing the level of eEF-2 kinase activity in a eukaryotic
2 cellular sample, comprising:

- 3 A. a predetermined amount of a detectably labelled specific binding
4 partner of eEF-2 kinase.
5 B. other reagents; and,
6 C. directions for use of said kit.

1 31. The test kit of Claim 31 wherein said labeled immunochemically reactive
2 component is selected from the group consisting of polyclonal antibodies to eEF-2
3 kinase, monoclonal antibodies to eEF-2 kinase, fragments thereof, and mixtures
4 thereof.

1 32. A method of preventing and/or treating cellular debilitations, derangements
2 and/or dysfunctions and/or other disease states in mammals, comprising
3 administering to a mammal a therapeutically effective amount of a material selected
4 from the following group:

- 5 A. peptides that inhibit eEF-2 kinase;
6 B. antibodies against eEF-2 kinase; and,
7 C. other drugs or agents that specifically inhibit eEF-2 kinase.

1 33. A pharmaceutical composition for the treatment of cellular debilitation,
2 derangement and/or dysfunction in mammals, comprising:

- 3 A. a therapeutically effective amount of a material selected from the
4 group consisting of: peptides that inhibit eEF-2 kinase; antibodies against eEF-2
5 kinase; and, other drugs or agents that specifically inhibit eEF-2 kinase; and,
6 B. a pharmaceutically acceptable carrier.

1 34. A recombinant virus transformed with the DNA molecule, or a derivative or
2 fragment thereof, in accordance with Claim 18.

1 35. A recombinant virus transformed with the DNA molecule, or a derivative or
2 fragment thereof, in accordance with Claim 19.

1 36. The recombinant DNA molecule of Claim 20 comprising plasmid pGEX-3X,
2 clone E3 or plasmid pGEX-3X, clone E4.

1 37. An antisense nucleic acid against eEF-2 kinase mRNA comprising a nucleic
2 acid sequence hybridizing to said mRNA.

1 38. The antisense nucleic acid of Claim 37 which is RNA.

1 39. The antisense nucleic acid of Claim 37 which is DNA.

1 40. The antisense nucleic acid of Claim 37 which binds to the initiation codon of
2 any of said mRNAs.

1 41. A recombinant DNA molecule having a DNA sequence which, on
2 transcription, produces an antisense ribonucleic acid against eEF-2 kinase mRNA,
3 said antisense ribonucleic acid comprising an nucleic acid sequence capable of
4 hybridizing to said mRNA.

1 42. A eEF-2 kinase-producing cell line transfected with the recombinant DNA
2 molecule of Claim 41.

1 43. A method for creating a cell line which exhibits reduced expression of eEF-
2 kinase, comprising transfecting a eEF-2 kinase-producing cell line with a
3 recombinant DNA molecule of claim 41.

1 44. A ribozyme that cleaves eEF-2 kinase mRNA.

1 45. The ribozyme of Claim 44 which is a *Tetrahymena*-type ribozyme.

1 46. The ribozyme of Claim 44 which is a Hammerhead-type ribozyme.

1 47. A recombinant DNA molecule having a DNA sequence which, upon
2 transcription, produces the ribozyme of claim 44.

1 48. A eEF-2 kinase-producing cell line transfected with the recombinant DNA
2 molecule of claim 47.

1 49. A method for creating a cell line which exhibits reduced expression of eEF-2
2 kinase, comprising transfecting a eEF-2 kinase-producing cell line with the
3 recombinant DNA molecule of claim 44.

1 50. An isolated nucleic acid encoding a protein kinase which is a member of a
2 superfamily, said protein kinase being characterized by: A. greater than 40%
3 sequence similarity with eEF-2 kinase from any organism; and, B. phosphorylates an
4 amino acid within an alpha helical domain of its target protein.

- 1 51. The isolated nucleic acid of claim 50, wherein the nucleic acid encodes eEF-
- 2 2 kinase protein, heart protein kinase, melanoma protein protein, or ch4 protien
- 3 kinase.



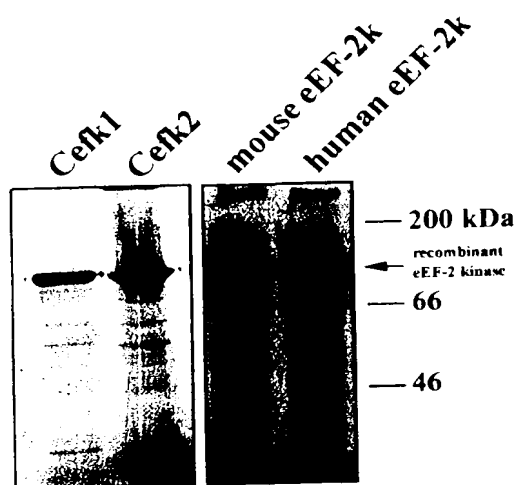


FIGURE 2

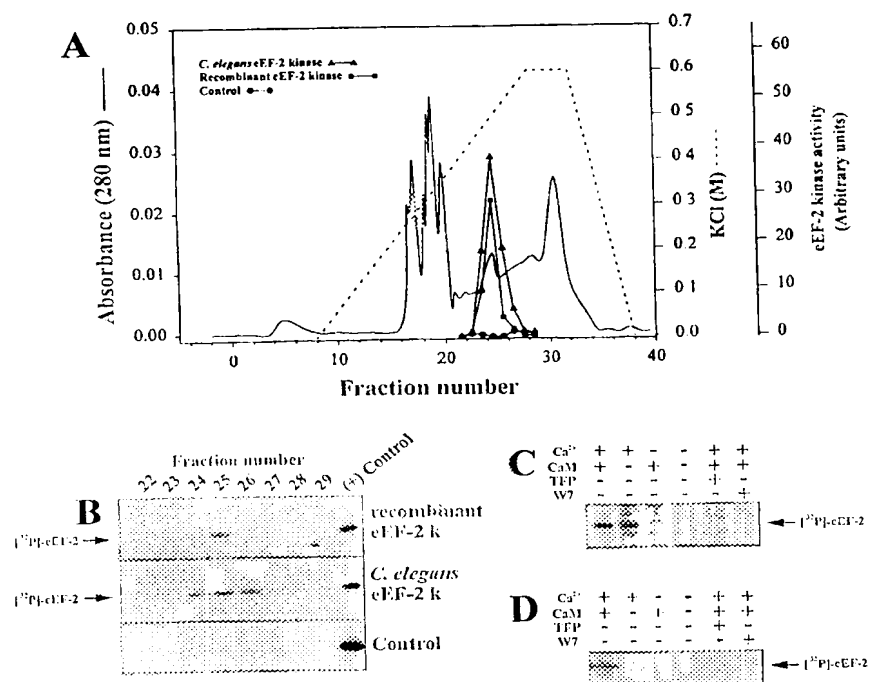


FIGURE 3

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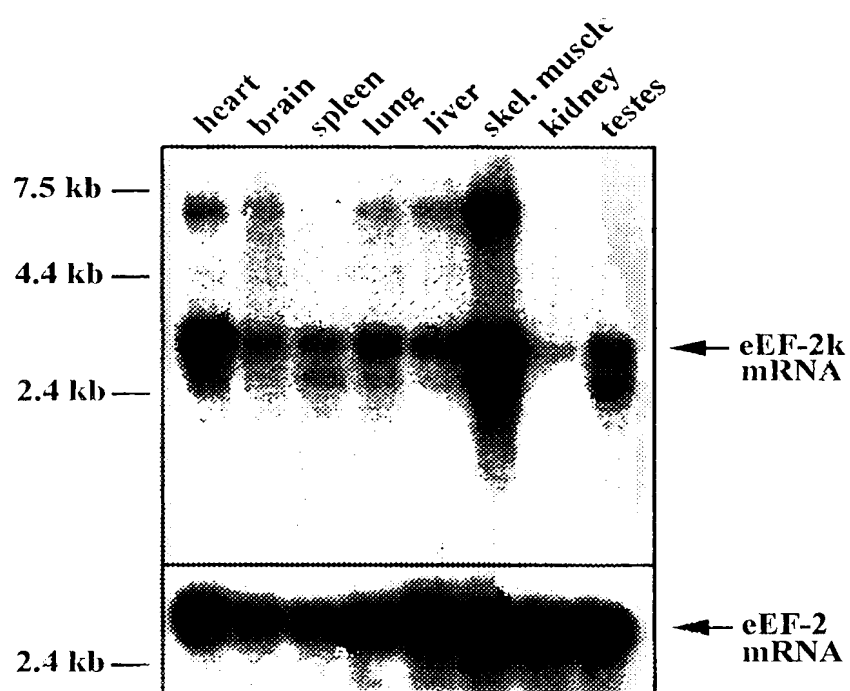


FIGURE 4

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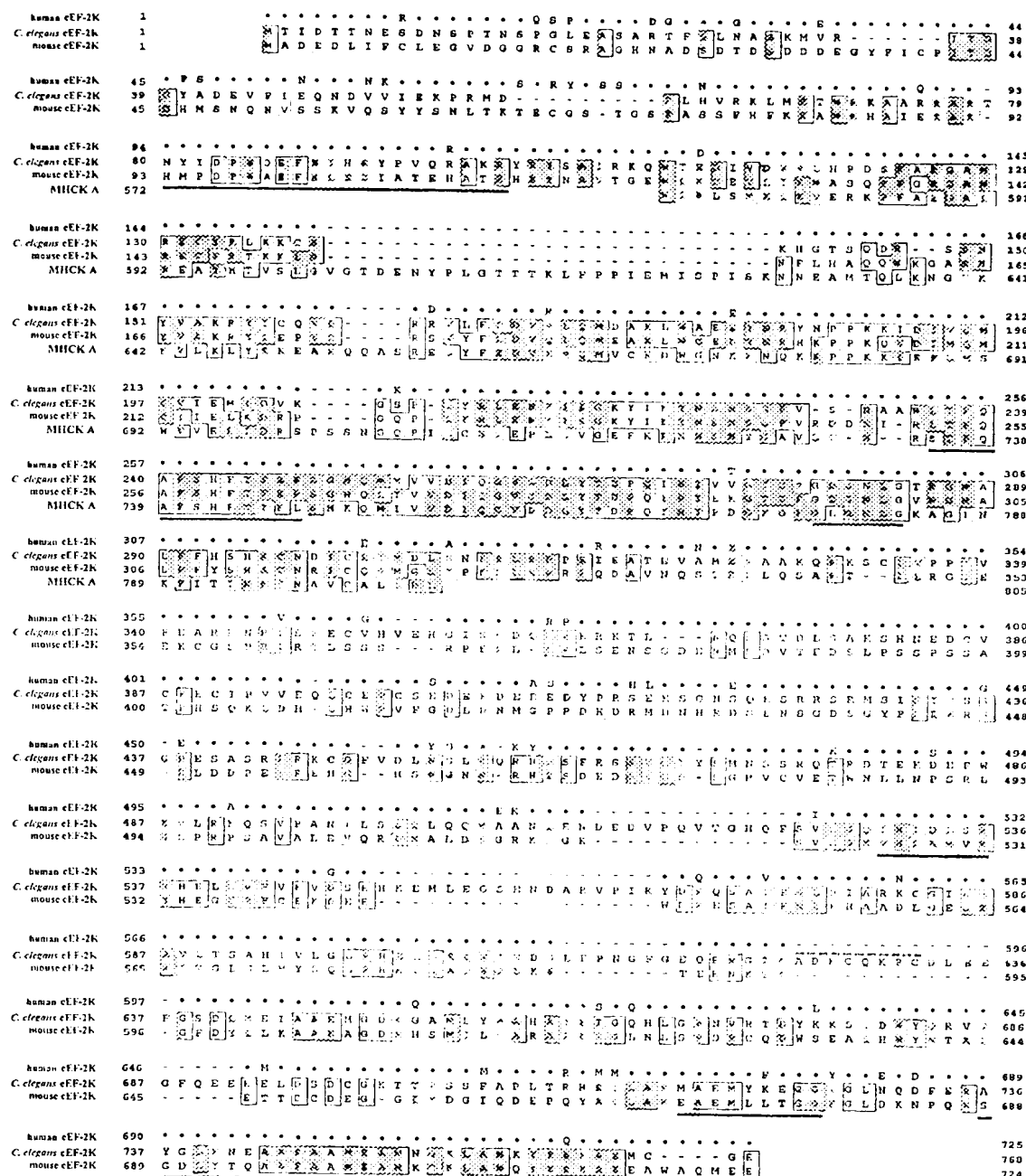


FIGURE 5

SUBSTITUTE SHEET (RULE 26)

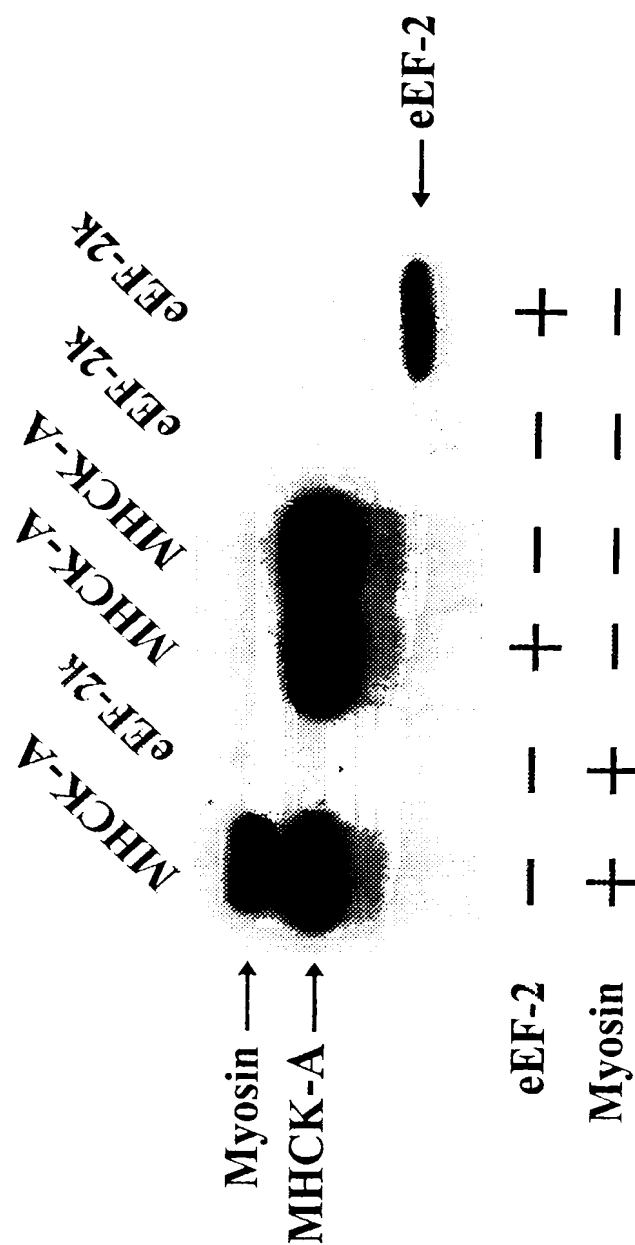


FIGURE 6

SUBSTITUTE SHEET (RULE 26)

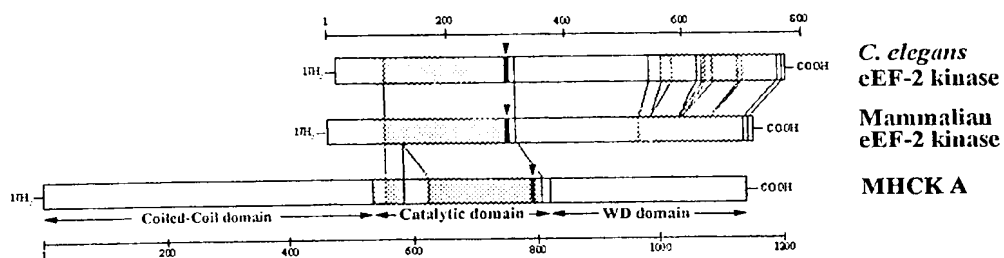


FIGURE 7

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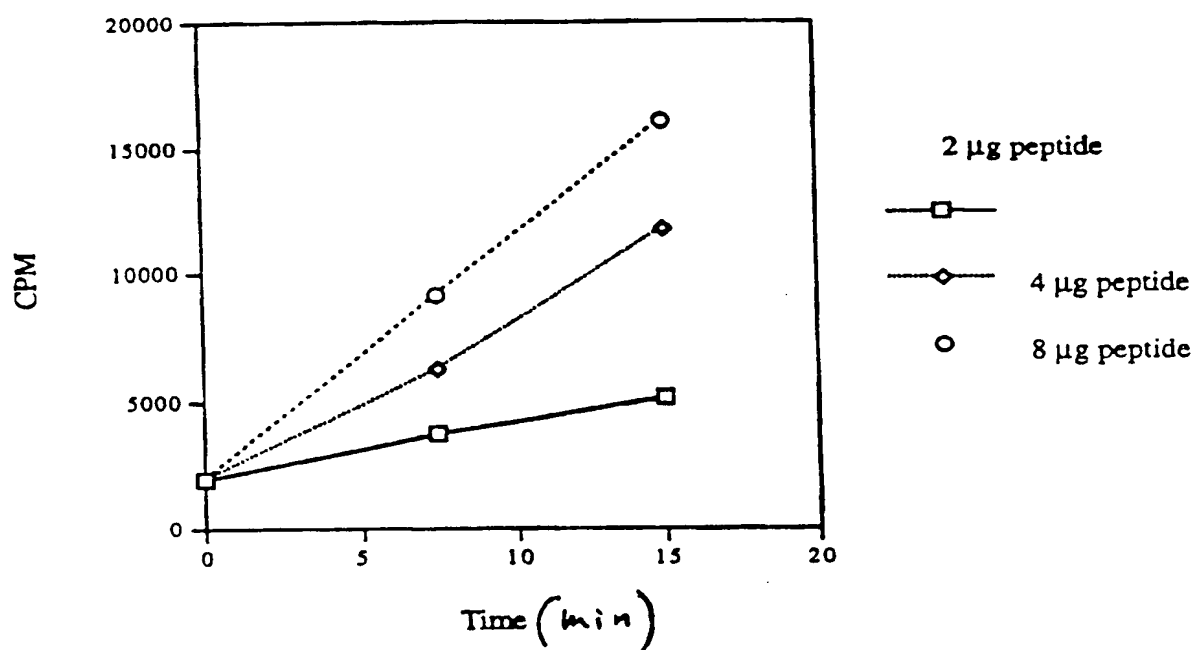


FIGURE 8

I		II	
H. EF2K	124	...F G M R F L	...Y V K Y
C.e. EF2K	110	...F G M R Y	...Y V K Y
MHCK A	572	...F G L R A Y	...F V K Y
MHCK B	132	...F G F R A Y	...Y V K Y
MHCK C	48	...F G R A H Y	...L V K
heart K	189	...F G H R A F	...V K H
melano K	48	...F G L R A Y	...Y V K Y
ch 4 K	1127	...F G R A F	...Y V K Y
consensus		...F G R A o	...o v k o
III		IV	
H. EF2K	178	...V V F D V L Q A W Y N	...L L E Y I G Y K Y N G V
C.e. EF2K	162	...V L F D V L Q A W Y N	...L L E F I G Y K Y N G V
MHCK A	653	...L Y F D V M Q A W Y N	...I E L L G F K N N G V
MHCK B	177	...V L F D V M Q A W Y N	...L L E Y V G Y K Y N G V
MHCK C	89	...V L F D V M Q A W Y N	...V E F I G Y K Y N G V
heart K	249	...V L F D V M Q A W Y N	...V E L G F K Y
melano K	108	...V L F D V M Q A W Y N	...V E M G F K Y N G V
ch 4 K	1173	...V L F D V M Q A W Y N	...V E Y I G F K L N G V
consensus		...V L F D V M Q A W Y N	...V E o o G o K o N G V
VI		VII	
H. EF2K	252	...F S H F F E S L L V D I Q G V	...L Y T D P Q I H
C.e. EF2K	235	...F S H F F E S L L V D I Q G V	...L Y T D P Q I H
MHCK A	734	...F S H F F E S L L V D I Q G V	...L Y T D P Q I H
MHCK B	254	...F S H F F E S L L V D I Q G V	...H Y T D P Q I H
MHCK C	165	...F S H F F E S L L V D I Q G V	...F Y T D P Q I H
heart K	335	...F S H F F E S L L V D I Q G V	...L T D I T
melano K	189	...F S H F F E S L L V D I Q G V	...L T D P V
ch 4 K	1253	...F S H F F E S L L V D I Q G V	...L T D P Q I H
consensus		...F S H F F E S L L V D I Q G V	...o o T D P Q I H
VIII		VIII	
H. EF2K	252	...F S H F F E S L L V D I Q G V	...L Y T D P Q I H
C.e. EF2K	235	...F S H F F E S L L V D I Q G V	...L Y T D P Q I H
MHCK A	734	...F S H F F E S L L V D I Q G V	...L Y T D P Q I H
MHCK B	254	...F S H F F E S L L V D I Q G V	...H Y T D P Q I H
MHCK C	165	...F S H F F E S L L V D I Q G V	...F Y T D P Q I H
heart K	335	...F S H F F E S L L V D I Q G V	...L T D I T
melano K	189	...F S H F F E S L L V D I Q G V	...L T D P V
ch 4 K	1253	...F S H F F E S L L V D I Q G V	...L T D P Q I H
consensus		...F S H F F E S L L V D I Q G V	...o o T D P Q I H

FIGURE 9

SUBSTITUTE SHEET (RULE 26)

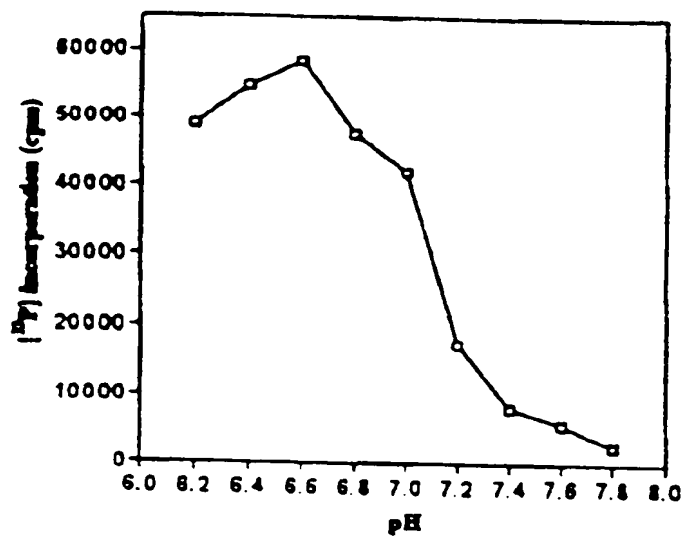


FIGURE 10

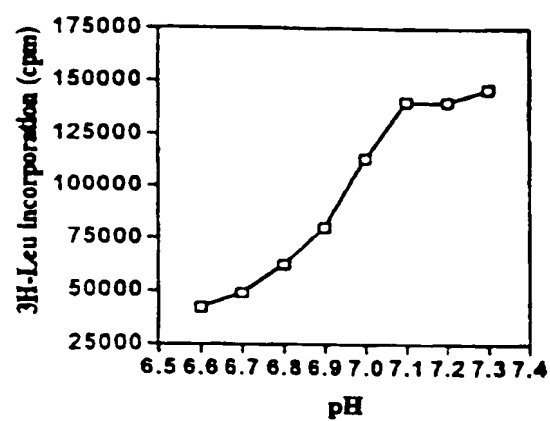


FIGURE 11

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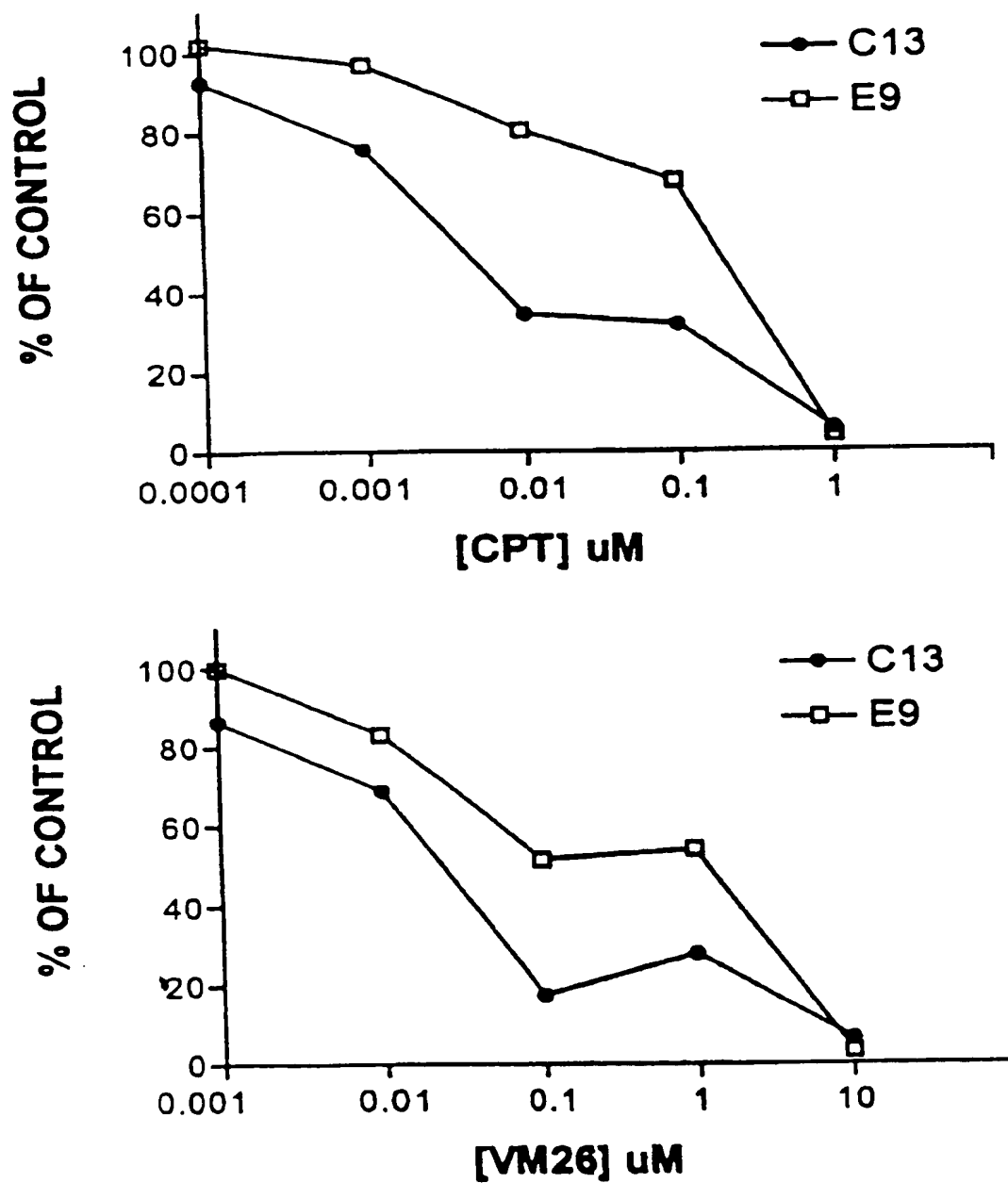


FIGURE 12

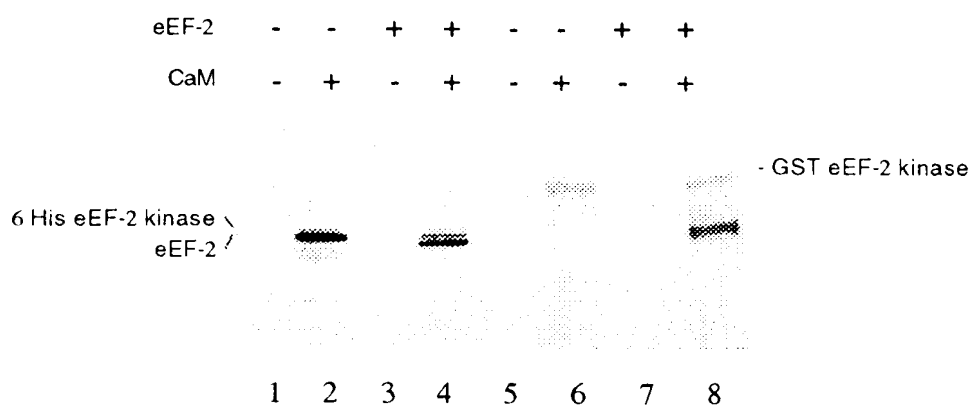


FIGURE 13

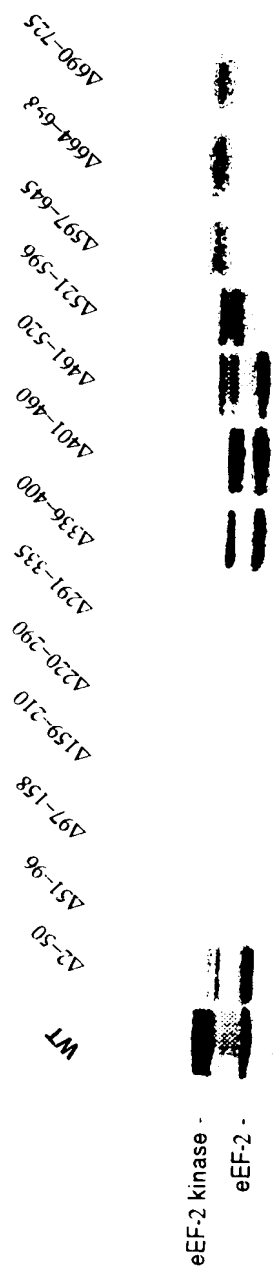


FIGURE 14

SUBSTITUTE SHEET (RULE 26)

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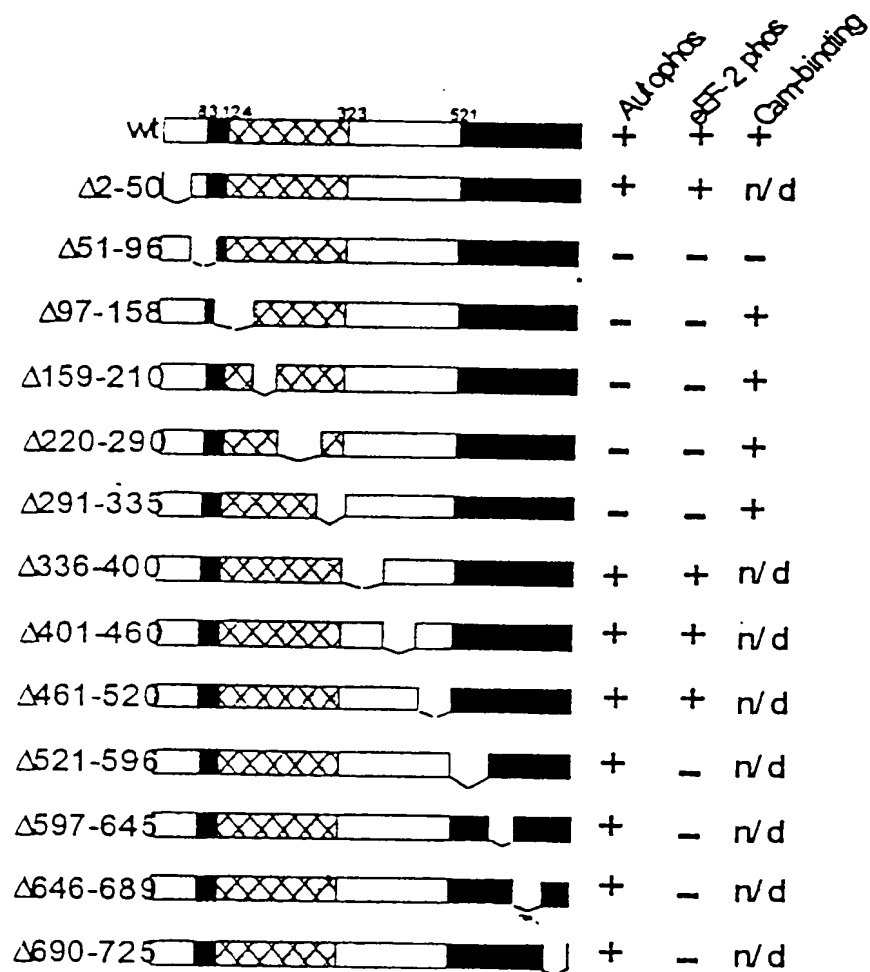
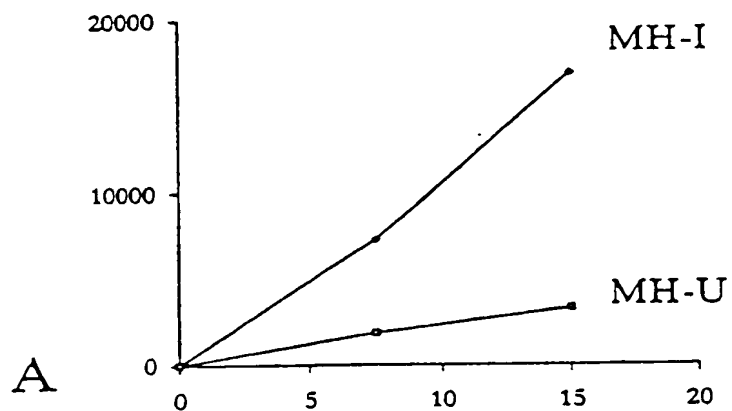


FIGURE 15

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*

RKKFGGESEKTKTKEFL - MHC
SARAGETRFTDTRKDE - EF2

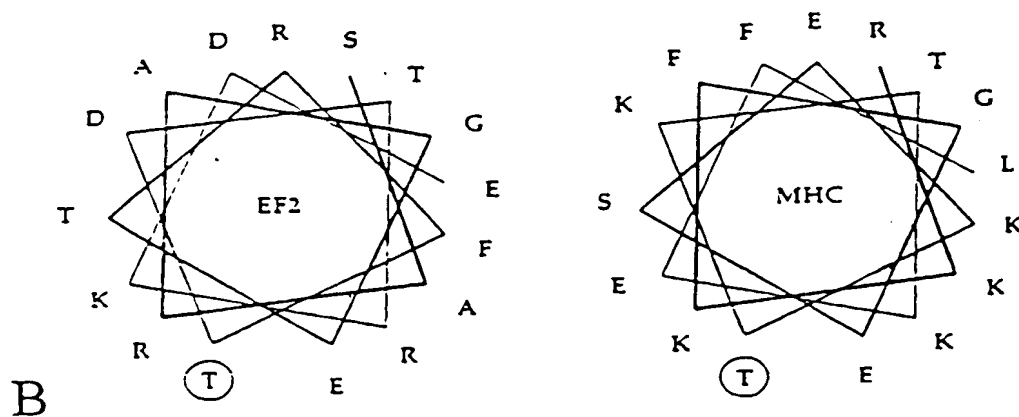


FIGURE 16

-1-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ryazanov, Alexey G.
Hait, William N.
Pavur, Karen S.
- (ii) TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
AND METHODS OF USE THEREFOR
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 601-1-078
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

-2-

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCAGACG AAGACCTCAT CTTCCGCCTG GAAGGTGTTG ATGGCGGCCA GTCCCCCGA	60
GCTGGCCATG ATGGTGATTC TGATGGGGAC AGCGACGATG AGGAAGGTTA CTTCATCTGC	120
CCCATCACGG ATGACCCAAG CTCGAACCAG AATGTCAATT CCAAGGTTAA TAAGTACTAC	180
AGCAACCTAA CAAAAAGTGA GCGGTATAGC TCCAGCGGGT CCCC GGCAAA CTCCTTCCAC	240
TTCAAGGAAG CCTGGAAGCA GCAATCCAG AAGGCCAAGC ACATGCCCGA CCCCTGGGCT	300
GAGTTCCACC TGGAAGATAT TCCACCGAA CGTGCTACTC GACACAGGTA CAACGCCGTC	360
ACCGGGGAAT GGCTGGATGA TGAAGTTCTG ATCAAGATGG CATCTCAGCC CTTGCGCCGA	420
GGAGCAATGA GGGAGTGCTT CCGGACGAAG AAGCTCTCCA ACTTCTTGCA TGCCCAGCAG	480
TGGAAGGGCG CCTCCAATA CGTGGCGAAG CGCTACATCG AGCCCGTAGA CCGGGATGTG	540
TACTTTGAGG ACGTGCGTCT ACAGATGGAG GCCAAGTCTT GGGGCGAGGA GTATAATCGG	600
CACAAGCCCC CCAAGCAGGT GGACATCATG CAGATGTGCA TCATCGAGCT GAAGGACAGA	660
CCGGGCAAGC CCCTCTTCCA CCTGGAGCAC TACATCGAGG GCAAGTACAT CAAGTACAAC	720
TCCAACCTCTG GCTTTGTCCG TGATGACAAC ATCCGACTGA CGCCGCAGGC CTTGAGCCAC	780
TTCACTTTTG AGCGTTCCGG CCATCAGCTG ATAGTGSTGG ACATCCAGGG AGTTGGGGAT	840
CTCTACACTG ACCCACAGAT CCACACGGAG ACGGGCACTG ACTTTGGAGA CGGCAACCTA	900
GGTGTCCGCG GGATGGCGCT CTTCTTCTAC TCTCATGCCT GCAACCGGAT TTGCGAGAGC	960
ATGGGCCTTG CTCCCTTTGA CCTCTCGCCC CGGGAGAGGG ATGCAGTGAA TCAGAACACC	1020
AAGCTGCTGC AATCAGCCAA GACCATCTTG AGAGGAACAG AGGAAAAATG TGGGAGCCCC	1080
CGAGTAAGGA CCCTCTCTGG GAGCCGGCCA CCCCTGCTCC GTCCCTTTC AGAGAACTCT	1140
GGAGACGAGA ACATGAGCGA CGTGACCTTC GACTCTCTCC CTTCTTCCCC ATCTTCGGCC	1200

-3-

ACACCACACA GCCAGAAGCT AGAGCACCTC CATTGBCACB TGTTCAGTGA CCTCGATAAC	1260
ATGGCATCCA GAGACCATGA TCATCTAGAC AAGCACCGGG AGTCTGAGAA TAGTGGGGAC	1320
AGCGGATACC CCAGTGAGAA GCGGGGTGAG CTGGATGACC CTGAGCCCCG AGAACATGGC	1380
CACTCATACA GTAATCGGAA GTACGAGTCT GACGAAGACA GCCTGGGCAG CTCTGGACGG	1440
GTATGTGTAG AGAAGTGGA TCTCCTCAAC TCCTCCCGCC TCCACCTGCC GAGGGCTTCG	1500
GCCGTGGCCC TGGAAAGTGCA AAGGCTTAAT GCTCTGGACC TCGAAAAGAA AATCGGGAAG	1560
TCCATTTTGG GGAAGGTCCA TCTGGCCATG GTGCGCTACC ACGAGGGTGG GCGCTTCTGC	1620
GAGAAGGGCG AGGAGTGGA CCAGSAGTCG GCTGTCTTCC ACCTGGAGCA CGCAGCCAAC	1680
CTGGGCGAGC TGGAGGCCAT CSTGGGCCTG GGA CTCTATGT ACTCGCAGTT GCCTCATCAC	1740
ATCCTAGCCG ATGTCTCTCT GAAGGAGACA GAAGAGAACA AAACCAAAGG ATTTGATTAC	1800
TTACTAAAGG CCGCTGAAGC TGGCGACAGG CAGTCCATGA TCCTAGTGGC GCGAGCTTTT	1860
GA CTCTGGCC AGAACCTCAG CCCGGACAGG TGCCAAGACT GGCTAGAGGC CCTGCACTGG	1920
TACAACACTG CCCTGGAGAT GACGGACTGT GATGAGGGCG GTGAGTACGA CGGAATGCAG	1980
GACGAGCCCC GGTACATGAT GTTGGCCAGG GAGGCAGAGA TGCTGTTTAC AGGAGGCTAC	2040
GGGCTGGAGA AGGACCCGCA GAGATCAGGG GACTTGTATA CCCAGGCAGC AGAGGCAGCG	2100
ATGGAAGCCA TGAAGGGCCG ACTGGCCAAC CAGTACTACC AAAAGGCTGA AGAGGCCTGG	2160
GCCCAGATGG AGGAATAA	2178

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

-4-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Asp	Glu	Asp	Leu	Ile	Phe	Arg	Leu	Glu	Gly	Val	Asp	Gly	Gly	1	5	10	15
Gln	Ser	Pro	Arg	Ala	Gly	His	Asp	Gly	Asp	Ser	Asp	Gly	Asp	Ser	Asp	20	25	30	
Asp	Glu	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp	Asp	Pro	Ser	Ser	35	40	45	
Asn	Gln	Asn	Val	Asn	Ser	Lys	Val	Asn	Lys	Tyr	Tyr	Ser	Asn	Leu	Thr	50	55	60	
Lys	Ser	Glu	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala	Asn	Ser	Phe	His	65	70	75	80
Phe	Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Gln	Lys	Ala	Lys	His	Met	Pro	85	90	95	
Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala	Thr	Glu	Arg	Ala	100	105	110	
Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp	Leu	Asp	Asp	Glu	115	120	125	
Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg	Gly	Ala	Met	Arg	130	135	140	
Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu	His	Ala	Gln	Gln	145	150	155	160
Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr	Ile	Glu	Pro	Val	165	170	175	
Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	Arg	Leu	Gln	Met	Glu	Ala	Lys	180	185	190	
Leu	Trp	Gly	Glu	Glu	Tyr	Asn	Arg	His	Lys	Pro	Pro	Lys	Gln	Val	Asp	195	200	205	
Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	Lys	Asp	Arg	Pro	Gly	Lys	Pro	210	215	220	
Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr	Ile	Lys	Tyr	Asn	225	230	235	240
Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg	Leu	Thr	Pro	Gln	245	250	255	
Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	Gln	Leu	Ile	Val				

-5-

260	265	270
Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His		
275	280	285
Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu Gly Val Arg Gly		
290	295	300
Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Glu Ser		
305	310	315
Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu Arg Asp Ala Val		
325	330	335
Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly		
340	345	350
Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr Leu Ser Gly Ser		
355	360	365
Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser Gly Asp Glu Asn		
370	375	380
Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser Pro Ser Ser Ala		
385	390	395
Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp Pro Val Phe Ser		
405	410	415
Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His Leu Asp Asn His		
420	425	430
Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro Ser Glu Lys Arg		
435	440	445
Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly His Ser Tyr Ser		
450	455	460
Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly Ser Ser Gly Arg		
465	470	475
Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser Arg Leu His Leu		
485	490	495
Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg Leu Asn Ala Leu		
500	505	510
Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly Lys Val His Leu		
515	520	525
Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys Glu Lys Gly Glu		

-6-

530	535	540
Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu His Ala Ala Asn		
545	550	555 560
Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Gln		
	565	570 575
Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu		
	580	585 590
Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly		
	595	600 605
Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe Asp Ser Gly Gln		
	610	615 620
Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu Ala Leu His Trp		
	625	630 635 640
Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu Gly Gly Glu Tyr		
	645	650 655
Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu Ala Arg Glu Ala		
	660	665 670
Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys Asp Pro Gln Arg		
	675	680 685
Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala Met Glu Ala Met		
	690	695 700
Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala Glu Glu Ala Trp		
	705	710 715 720
Ala Gln Met Glu Glu		
	725	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCAGACG AAGACCTCAT CTTCTGCCTG GAAGGTGTTG ACGGTGGCAG GTGCTCCCGA	60
GCTGSCCACA ATGCGGACTC TGACACAGAC AGTGAAGATG ATGAGGGCTA TTTCATCTGC	120
CCCATCACTG ATGACCACAT GTCCAATCAG AATGTGAGCT CCAAAGTCCA GAGCTACTAT	180
AGCAACCTAA CAAAAACAGA GTGCGGCTCC ACAGGCTCAC CAGCCAGCTC CTTCCACTTC	240
AAGGAAGCCT GGAAGCATGC GATCGAGAAA GCCAAGCACA TGCCTGACCC CTGGGCTGAA	300
TTCCATCTCG AGGACATCGC CACAGAACAT GCTACTCGGC ACAGGTACAA CGCTGTCACC	360
GGGGAATGGC TGAAAGACGA GGTTCCTGATC AAGATGGCGT CTCAGCCCTT CGGCCGTGGA	420
GCAATGAGGG AGTGCTTCAG GACGAAGAAA CTCTCCAACT TCTGACACGC CCAGCAATGG	480
AAGGGGGCCT CCAACTACCT GSCCAAGCGC TACATCGAGC CGGTGGACAG GAGCGTGTAC	540
TTTGAGGATG TGCAGCTCCA GATGGAGGCG AAGCTCTGGG GGGAGGATTA CAATCGGCAC	600
AAGCCCCCCA AGCAGGTGGA TATCATGCAG ATGTGCATCA TTGAGCTAAA GGACAGACCA	660
GGCCAGCCCC TCTTCCACTT GGAGCACTAC ATTGAGGGCA AGTACATCAA GTACAATTCC	720
AACTCAGGCT TTGTCCGTGA TGACAACATC CGACTAACCC CACAGGCCTT CAGCCATTTC	780
ACATTTGAGC GTTCTGGTCA TCAGCTGATT GTAGTGGACA TCCAGGGTGT GGGTGACCTT	840
TATACCGACC CACAGATCCA CACTGAGAAA GGCAGTGAAT TTGAGATGG TAACCTTGGT	900
GTCCGGGGAA TGGCTCTCTT CTTCTACTCT CATGCCTGCA ACCGGATTTG TCAGAGCATG	960
GGCCTTACGC CCTTTGACCT CTCCCCACGG GAACAGGATG CGGTGAATCA GAGCACCAGG	1020
CTATTGCAAT CAGCCAAGAC CATCTTGAGG GGGACAGAGG AGAAGTGTGG GAGTCCCCGC	1080
ATAAGGACAC TCTCTAGCAG CCGGCCCCCT TTGCTCCTTC GCCTGTCAGA GAACTCCGGG	1140
GATGAGAACA TGAGTGACGT GACCTTTGAC TCTCTGCCTT CCTCCCCGTC TTCAGCTACA	1200
CCACACAGCC AGAAACTGGA CCACCTCCAT TGGCCAGTGT TTGGTGACCT CGATAACATG	1260
GGCCCTAGAG ACCATGACCG TATGGACAAT CACCGGGAAT CTGAGAATAG TGGGGACAGT	1320
GGGTATCCAA GCGAGAAGCG AAGTGACCTG GATGATCCTG AGCCCCGAGA ACACGGCCAC	1380

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TCCAACGGCA ACCGAAGGCA TGAATCTGAC GAGGATAGCC TGGGCAGCTC TGGACGGGTC      1440
TGTGTGGAGA CGTGGAACCT GGTCAATCCC TCCCGCCTGC ACCTGCCGAG GCCCTCGGCC      1500
GTGGCCCTAG AAGTGCAGAG GCTAAATGCC CTGGACCTTG GAAGGAAAAT CGGGAAGTCT      1560
GTTTTGGGGA AAGTCCATTT GGCCATGGTG CGATACCACG AGGGCGGGCG CTTCTGCGAG      1620
AAGGATGAGG AGTGGGATCG AGAGTCAGCC ATCTTCCATC TGGAGCATGC AGCTGACCTG      1680
GGAGAACTGG AGGCCATCGT GGGCCTAGGC CTCATGTACT CTCAGCTGCC CCACCACATC      1740
CTGGCTGATG TCTCTCTGAA GGAGACAGAG GAGAACAAGA CAAAAGGCTT TGATTACTTA      1800
CTGAAGGCGG CAGAAGCTGG TGACAGGCAT TCCATGATTT TAGTGGCCCG AGCTTTTGAC      1860
ACTGGCCTGA ACCTCAGCCC AGACAGGTGT CAAGACTGGT CGGAAGCCTT GCACTGGTAC      1920
AACACAGCCC TGGAGACAAC AGACTGCGAT GAAGGCGGGG AGTACGATGG GATACAGGAC      1980
GAGCCCCAGT ACGCACTGCT GGGCAGGGAG GCGGAGATGC TGCTCACCAG GGGATTTGGA      2040
CTGGACAAGA ACCCCCCAAG ATCAGGAGAT TTGTACACCC AGGCAGCTGA GGCAGCAATG      2100
GAAGCCATGA AGGGCCGGCT AGCCAACCAG TACTACGAGA AGGCGGAAGA GGCCTGGGCC      2160
CAGATGGAGG AATAA                                           2175

```

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ala Asp Glu Asp Leu Ile Phe Cys Leu Glu Gly Val Asp Gly Gly
1           5           10          15

Arg Cys Ser Arg Ala Gly His Asn Ala Asp Ser Asp Thr Asp Ser Asp

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BNSDOCID: <WO__9909199A2_1_>

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290	295	300
Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Gln Ser Met		
305	310	315 320
Gly Leu Thr Pro Phe Asp Leu Ser Pro Arg Glu Gln Asp Ala Val Asn		
	325	330 335
Gln Ser Thr Arg Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly Thr		
	340	345 350
Glu Glu Lys Cys Gly Ser Pro Arg Ile Arg Thr Leu Ser Ser Ser Arg		
	355	360 365
Pro Pro Leu Leu Leu Arg Leu Ser Glu Asn Ser Gly Asp Glu Asn Met		
	370	375 380
Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser Pro Ser Ser Ala Thr		
	385	390 395 400
Pro His Ser Gln Lys Leu Asp His Leu His Trp Pro Val Phe Gly Asp		
	405	410 415
Leu Asp Asn Met Gly Pro Arg Asp His Asp Arg Met Asp Asn His Arg		
	420	425 430
Asp Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro Ser Glu Lys Arg Ser		
	435	440 445
Asp Leu Asp Asp Pro Glu Pro Arg Glu His Gly His Ser Asn Gly Asn		
	450	455 460
Arg Arg His Glu Ser Asp Glu Asp Ser Leu Gly Ser Ser Gly Arg Val		
	465	470 475 480
Cys Val Glu Thr Trp Asn Leu Leu Asn Pro Ser Arg Leu His Leu Pro		
	485	490 495
Arg Pro Ser Ala Val Ala Leu Glu Val Gln Arg Leu Asn Ala Leu Asp		
	500	505 510
Leu Gly Arg Lys Ile Gly Lys Ser Val Leu Gly Lys Val His Leu Ala		
	515	520 525
Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys Glu Lys Asp Glu Glu		
	530	535 540
Trp Asp Arg Glu Ser Ala Ile Phe His Leu Glu His Ala Ala Asp Leu		
	545	550 555 560
Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Gln Leu		

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	565		570		575
Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu Asn					
	580		585		590
Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly Asp					
	595		600		605
Arg His Ser Met Ile Leu Val Ala Arg Ala Phe Asp Thr Gly Leu Asn					
	610		615		620
Leu Ser Pro Asp Arg Cys Gln Asp Trp Ser Glu Ala Leu His Trp Tyr					
	625		630		635
Asn Thr Ala Leu Glu Thr Thr Asp Cys Asp Glu Gly Gly Glu Tyr Asp					
	645		650		655
Gly Ile Gln Asp Glu Pro Gln Tyr Ala Leu Leu Ala Arg Glu Ala Glu					
	660		665		670
Met Leu Leu Thr Gly Gly Phe Gly Leu Asp Lys Asn Pro Gln Arg Ser					
	675		680		685
Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala Met Glu Ala Met Lys					
	690		695		700
Gly Arg Leu Ala Asn Gln Tyr Tyr Glu Lys Ala Glu Glu Ala Trp Ala					
	705		710		715
					720
Gln Met Glu Glu					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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ATGTTTAATA TAAAAAGAG AAAAGAGAGT ATAACAGGTA TACCACCAAT AAATGTTAAT 60
AGTCCACAAT CAGTTCCATT GAGTGGAACA TTGCAATCAC CATTGATTAC ACCAAATTCA 120
CCAAATTTTG TTTCACGTCA ATGTCCATTC AAAAAGTTTG GATGTAGTAG TTTTITAGTT 180
TCAAAGGCAG AGTTTGATAA TCACTTAAAG GATGACGCAC AATTTCATTT ACAATTGGCA 240
GTGGAGAAAT TTGATCATCA ATTTGATTTA CACACACAAT TGATGGCACA TTTTACTGAG 300
CAAATGGAGG ATCAATTAGA GAAAACAATG AAGGTCGTAC GTAATCATAC AGATAGTTTA 360
GGCGTAATG TTCAAACCAA ATTGATGAA GGCATTGAAA AATGTATGGC TTTTGCTAAA 420
AAGGTTGAAC AACAACAACA ACAATTGGCC AAAAGATTAA TCACTCAACA AATTCAAGAG 480
AAGAAATCAA CCTCTTCACC TTTAGTTAAA GGTGGTATTA GTGGTGGTGG TGGTAGTGGT 540
GGCGATGATT CTTTTGATGG CGCAAATATA TCATCAATGT CAACTAGTAA ACAAGAATTA 600
CAACAAGAAT TACAATCATT ATCAATTAAA ATGAAAAAAG AATTGACAGA ATTATCCGAT 660
GAACTATCAC AAAAATTAGA AGGTTCAACA GGTAATATAG ATATTAAAAT AAAGAGAATC 720
GAAGGTGAAG TTAATGAAAA GATTGATAAA CGTCAATTGG TCTCTACGAT CGATGATTCA 780
ATTGGAAAGA AAACAGATTC CATCGGTTAT ACATTGGAGA GTTCAATCAT TAAAAAGGTT 840
GAAGAGAAAG AGAAAAAGAA ATCCGAACAA AATCAACTTC TCTTTGATTC AAAGATTGAA 900
TCCTTAAAAG ATAAGATTAA AATCATTGAA ACTCAACAAT TGGATACTTC ATCAGAGGTT 960
AGAAAATTGA AATTAGAAAG TACAAGTAGT GGAAATTTAA TGGCAGGTCT TAATGGTACC 1020
TCTGGTAGAC CTTTCATCCT TTCTCACTTT ATTCCATCCT CTGTTTCTGC CGCTGCTAAC 1080
AATATCAACA AGAATGAAAT CATGGAAGAG GTTAAAAAGG TAGAAGAGAA ACTTCAAAAG 1140
AAAATTCGTG AAGAGATTGA TAATACAAAA GCTGAACTCT CAAAGGTTGA ACGTTCCGTT 1200
AAAGATAATC GTAGTGAAAT TGAAGGTTTG GAAAAAGATT GTAAGAATCA ATTCGATAAA 1260
CAAGACAATA AGATCAAACA AGTTGAGGAT GATTTGAAAA AGAGTGATTC ATTACTTTTG 1320
TTAATGCAAA ATAACCTCAA GAAATATAAT GAATTTGTTG ATAGAGAACG TGATCGTGAA 1380
AGTGAACGTT TGAAACTTCA AGATTCTATC AAACGTTTAG AACAAAATCA AAAGAAAATC 1440
GAAGCTGAAA TTCAAGAAGG TAATGAACAA GTTGAACGTG TTTTACGTGA GGAAGCTTCA 1500
ATCTCACCAA TTAGTTCAGT TCCAAAATCA CCAATCACAA CCAAACGTTT ATCGATTATT 1560

TTAAATTCAC CACCAATGAC TTCACAACAA TCATCACCAA AGATTCAAGA TCTTCTCTCA 1620
AGTAGTGGTA GTAGTAGTGT TAGTGGTATA AATATTTCTT CTGAAACCGG TGAAATGGGT 1680
ATTCTTTGGG AATTTGATCC AATCATTAAC AAATGGATTA GATTATCAAT GAAGCTAAAG 1740
GTAGAAAGAA AACCATTGTC AGAGGGTGCT CTTAGAGAGG CTTATCATAC CGTTTCATTG 1800
GGTGTGGAA CCGATGAAAA TTATCCATTA GGTACAACCA CCAAATTATT CCCACCAATT 1860
GAAATGATTT CACCAATTTT AAAGAATAAT GAGGCAATGA CTCAATTGAA GAATGGTACA 1920
AAATTTGTTT TGAAACTCTA CAAAAGGAA GCTGAACAAC AAGCTAGCAG AGAATTATAC 1980
TTTGAAGATG TTAAAATGCA AATGGTCTGT AGAGATTGGG GTAATAAATT CAATCAAAAG 2040
AAACCACCAA AGAAAATTGA ATTCCTTATG TCTTGGGTTG TAGAGTTAAT CGATAGATCT 2100
CCTTCTTCCA ATGGTCAACC AATACTTTGT TCCATTGAAC CATTATTGGT TGGTGAATTC 2160
AAAAAGAATA ATTCAAATTA TGGTGCAGTT TTAACCAATC GTTCAACTCC ACAAGCATTC 2220
TCTCATTTCA CCTATGAACT CTCAAATAAA CAAATGATCG TTGTCGATAT TCAAGGTGTT 2280
GATGATCTTT AACTGATCC TCAAATTCAT ACACCCGATG GTAAAGGATT TGGTCTTGGT 2340
AATCTTGGTA AAGCAGGTAT CAATAAATTC ATCACCACCT ACAAAATGTAA TGCTGTTTGT 2400
GCTCTTTTAG ATTTAGATGT TAAATTGGGT GGTGTACTAT CTGGAAATAA TAAGAAACAA 2460
CTTCAACAAG GTACTATGGT TATGCCAGAT ATTCTCCCAG AACTTATGCC ATCTGATAAC 2520
ACCATTAAG TGGGTGCAAA ACAACTTCCA AAAGCTGAAT TCTCAAAGAA AGATCTCAAA 2580
TGTGTTAGCA CCATTCAAAG TTTCCGTGAA CGTGTTAACT CGATCGCATT CTTTGATAAT 2640
CAAAAGTTAT TATGCGCTGG TTATGGTGAT GGTACCTATA GAGTTTTCGA TGTCAATGAC 2700
AATTGGAAAT GTTTATACAC TGTCAATGGT CATAGAAAAT CAATTGAAAG TATCGCTTGT 2760
AATAGTAATT ACATTTTTCAC TTCATCACCT GATAACACCA TCAAAGTTCA TATCATTCTG 2820
AGTGSTAACA CCAAATGTAT AGAGACATTG GTTGGTCACA CTGGTGAAGT TAATTGTGTC 2880
GTGGCCAATG AAAAAATATCT TTTCAAGTTGT AGTTATGATA AAATATCAA GGTGTTGGAT 2940
TTGTCAACCT TTAAAGAAAT TAAATCATTT GAGGGTGTTT ATACAAAGTA CATTAAACA 3000
TTGGCTTTGA GTGGACGTTA TCTTTTGTAG GGTGGTAACG ATCAAATCAT TTACGTTTGG 3060
GATACTGAAA CACTTAGTAT GCTTTTCAAT ATGCAAGGTC ATGAAGATTG GGTACTCTCT 3120

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CTTCATTGTA CCGCTAGTTA TETTTTCTCA ACCTCAAAAG ATAATGTCAT CAAGATTTGG 3180
 GATCTCTCAA ATTCAGTTG TATCGATACT CTAAAAGGTC ATTGGAATTC TGTCTCAAGT 3240
 TGTGTCGTAA AAGATCGTTA TCTATACAGT GGTTCTGAAG ATAATTCAAT CAAAGTTTGG 3300
 GATCTCGATA CACTTGAATG TGTTTACACC ATCCAAAAT CTCATTCTTT GGGTGTAATA 3360
 TGTTTAATGG TTTTCAATAA TCAAATCATT TCTGCTGCTT TCGATGGTTC AATTAAAGTT 3420
 TGGGAATGGC AATCGAAATA ATCTTTGTAA ATTTTGTTA AAAAA 3465

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Phe	Asn	Ile	Lys	Lys	Arg	Lys	Glu	Ser	Ile	Thr	Gly	Ile	Pro	Pro	1	5	10	15
Ile	Asn	Val	Asn	Ser	Pro	Gln	Ser	Val	Pro	Leu	Ser	Gly	Thr	Leu	Gln	20	25	30	
Ser	Pro	Leu	Ile	Thr	Pro	Asn	Ser	Pro	Asn	Phe	Val	Ser	Arg	Gln	Cys	35	40	45	
Pro	Phe	Lys	Lys	Phe	Gly	Cys	Ser	Ser	Phe	Leu	Val	Ser	Lys	Ala	Glu	50	55	60	
Phe	Asp	Asn	His	Leu	Lys	Asp	Asp	Ala	Gln	Phe	His	Leu	Gln	Leu	Ala	65	70	75	80
Val	Glu	Lys	Phe	Asp	His	Gln	Phe	Asp	Leu	His	Thr	Gln	Leu	Met	Ala	85	90	95	
His	Phe	Thr	Glu	Gln	Met	Glu	Asp	Gln	Leu	Glu	Lys	Thr	Met	Lys	Val	100	105	110	

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Val	Arg	Asn	His	Thr	Asp	Ser	Leu	Gly	Gly	Asn	Val	Gln	Thr	Lys	Leu	115	120	125	
Asp	Glu	Gly	Ile	Glu	Lys	Cys	Met	Ala	Phe	Ala	Lys	Lys	Val	Glu	Gln	130	135	140	
Gln	Gln	Gln	Gln	Leu	Ala	Lys	Arg	Leu	Ile	Thr	Gln	Gln	Ile	Gln	Glu	145	150	155	160
Lys	Lys	Ser	Thr	Ser	Ser	Pro	Leu	Val	Lys	Gly	Gly	Ile	Ser	Gly	Gly	165	170	175	
Gly	Gly	Ser	Gly	Gly	Asp	Asp	Ser	Phe	Asp	Gly	Ala	Asn	Ile	Ser	Ser	180	185	190	
Met	Ser	Thr	Ser	Lys	Gln	Glu	Leu	Gln	Gln	Glu	Leu	Gln	Ser	Leu	Ser	195	200	205	
Ile	Lys	Met	Lys	Lys	Glu	Leu	Thr	Glu	Leu	Ser	Asp	Glu	Leu	Ser	Gln	210	215	220	
Lys	Leu	Glu	Arg	Ser	Thr	Gly	Asn	Ile	Asp	Ile	Lys	Ile	Lys	Arg	Ile	225	230	235	240
Glu	Gly	Glu	Val	Asn	Glu	Lys	Ile	Asp	Lys	Arg	Gln	Leu	Val	Ser	Thr	245	250	255	
Ile	Asp	Asp	Ser	Ile	Gly	Lys	Lys	Thr	Asp	Ser	Ile	Gly	Tyr	Thr	Leu	260	265	270	
Glu	Ser	Ser	Ile	Ile	Lys	Lys	Val	Glu	Glu	Lys	Glu	Lys	Lys	Lys	Ser	275	280	285	
Glu	Gln	Asn	Gln	Leu	Leu	Phe	Asp	Ser	Lys	Ile	Glu	Ser	Leu	Lys	Asp	290	295	300	
Lys	Ile	Lys	Ile	Ile	Glu	Thr	Gln	Gln	Leu	Asp	Thr	Ser	Ser	Glu	Val	305	310	315	320
Arg	Lys	Leu	Lys	Leu	Glu	Ser	Thr	Ser	Ser	Gly	Asn	Leu	Met	Ala	Gly	325	330	335	
Leu	Asn	Gly	Thr	Ser	Gly	Arg	Pro	Ser	Ser	Ser	Ser	His	Phe	Ile	Pro	340	345	350	
Ser	Ser	Val	Ser	Ala	Ala	Ala	Asn	Asn	Ile	Asn	Lys	Asn	Glu	Ile	Met	355	360	365	
Glu	Glu	Val	Lys	Lys	Val	Glu	Glu	Lys	Leu	Gln	Lys	Lys	Ile	Arg	Glu	370	375	380	

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Glu Ile Asp Asn Thr Lys Ala Glu Leu Ser Lys Val Glu Arg Ser Val
 385 390 395 400
 Lys Asp Asn Arg Ser Glu Ile Glu Gly Leu Glu Lys Asp Cys Lys Asn
 405 410 415
 Gln Phe Asp Lys Gln Asp Asn Lys Ile Lys Gln Val Glu Asp Asp Leu
 420 425 430
 Lys Lys Ser Asp Ser Leu Leu Leu Leu Met Gln Asn Asn Leu Lys Lys
 435 440 445
 Tyr Asn Glu Phe Val Asp Arg Glu Arg Asp Arg Glu Ser Glu Arg Leu
 450 455 460
 Lys Leu Gln Asp Ser Ile Lys Arg Leu Glu Gln Asn Gln Lys Lys Ile
 465 470 475 480
 Glu Ala Glu Ile Gln Glu Gly Asn Glu Gln Val Glu Arg Val Leu Arg
 485 490 495
 Glu Glu Ala Ser Ile Ser Pro Ile Ser Ser Val Pro Lys Ser Pro Ile
 500 505 510
 Thr Thr Lys Arg Ser Ser Ile Ile Leu Asn Ser Pro Pro Met Thr Ser
 515 520 525
 Gln Gln Ser Ser Pro Lys Ile Gln Asp Leu Leu Ser Ser Ser Gly Ser
 530 535 540
 Ser Ser Val Ser Gly Ile Asn Ile Ser Ser Glu Thr Gly Glu Met Gly
 545 550 555 560
 Ile Leu Trp Glu Phe Asp Pro Ile Ile Asn Lys Trp Ile Arg Leu Ser
 565 570 575
 Met Lys Leu Lys Val Glu Arg Lys Pro Phe Ala Glu Gly Ala Leu Arg
 580 585 590
 Glu Ala Tyr His Thr Val Ser Leu Gly Val Gly Thr Asp Glu Asn Tyr
 595 600 605
 Pro Leu Gly Thr Thr Thr Lys Leu Phe Pro Pro Ile Glu Met Ile Ser
 610 615 620
 Pro Ile Ser Lys Asn Asn Glu Ala Met Thr Gln Leu Lys Asn Gly Thr
 625 630 635 640
 Lys Phe Val Leu Lys Leu Tyr Lys Lys Glu Ala Glu Gln Gln Ala Ser
 645 650 655

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Arg Glu Leu Tyr Phe Glu Asp Val Lys Met Gln Met Val Cys Arg Asp
660 665 670

Trp Gly Asn Lys Phe Asn Gln Lys Lys Pro Pro Lys Lys Ile Glu Phe
675 680 685

Leu Met Ser Trp Val Val Glu Leu Ile Asp Arg Ser Pro Ser Ser Asn
690 695 700

Gly Gln Pro Ile Leu Cys Ser Ile Glu Pro Leu Leu Val Gly Glu Phe
705 710 715 720

Lys Lys Asn Asn Ser Asn Tyr Gly Ala Val Leu Thr Asn Arg Ser Thr
725 730 735

Pro Gln Ala Phe Ser His Phe Thr Tyr Glu Leu Ser Asn Lys Gln Met
740 745 750

Ile Val Val Asp Ile Gln Gly Val Asp Asp Leu Tyr Thr Asp Pro Gln
755 760 765

Ile His Thr Pro Asp Gly Lys Gly Phe Gly Leu Gly Asn Leu Gly Lys
770 775 780

Ala Gly Ile Asn Lys Phe Ile Thr Thr His Lys Cys Asn Ala Val Cys
785 790 795 800

Ala Leu Leu Asp Leu Asp Val Lys Leu Gly Gly Val Leu Ser Gly Asn
805 810 815

Asn Lys Lys Gln Leu Gln Gln Gly Thr Met Val Met Pro Asp Ile Leu
820 825 830

Pro Glu Leu Met Pro Ser Asp Asn Thr Ile Lys Val Gly Ala Lys Gln
835 840 845

Leu Pro Lys Ala Glu Phe Ser Lys Lys Asp Leu Lys Cys Val Ser Thr
850 855 860

Ile Gln Ser Phe Arg Glu Arg Val Asn Ser Ile Ala Phe Phe Asp Asn
865 870 875 880

Gln Lys Leu Leu Cys Ala Gly Tyr Gly Asp Gly Thr Tyr Arg Val Phe
885 890 895

Asp Val Asn Asp Asn Trp Lys Cys Leu Tyr Thr Val Asn Gly His Arg
900 905 910

Lys Ser Ile Glu Ser Ile Ala Cys Asn Ser Asn Tyr Ile Phe Thr Ser
915 920 925

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Ser Pro Asp Asn Thr Ile Lys Val His Ile Ile Arg Ser Gly Asn Thr
 930 935 940

Lys Cys Ile Glu Thr Leu Val Gly His Thr Gly Glu Val Asn Cys Val
 945 950 955 960

Val Ala Asn Glu Lys Tyr Leu Phe Ser Cys Ser Tyr Asp Lys Thr Ile
 965 970 975

Lys Val Trp Asp Leu Ser Thr Phe Lys Glu Ile Lys Ser Phe Glu Gly
 980 985 990

Val His Thr Lys Tyr Ile Lys Thr Leu Ala Leu Ser Gly Arg Tyr Leu
 995 1000 1005

Phe Ser Gly Gly Asn Asp Gln Ile Ile Tyr Val Trp Asp Thr Glu Thr
 1010 1015 1020

Leu Ser Met Leu Phe Asn Met Gln Gly His Glu Asp Trp Val Leu Ser
 1025 1030 1035 1040

Leu His Cys Thr Ala Ser Tyr Leu Phe Ser Thr Ser Lys Asp Asn Val
 1045 1050 1055

Ile Lys Ile Trp Asp Leu Ser Asn Phe Ser Cys Ile Asp Thr Leu Lys
 1060 1065 1070

Gly His Trp Asn Ser Val Ser Ser Cys Val Val Lys Asp Arg Tyr Leu
 1075 1080 1085

Tyr Ser Gly Ser Glu Asp Asn Ser Ile Lys Val Trp Asp Leu Asp Thr
 1090 1095 1100

Leu Glu Cys Val Tyr Thr Ile Pro Lys Ser His Ser Leu Gly Val Lys
 1105 1110 1115 1120

Cys Leu Met Val Phe Asn Asn Gln Ile Ile Ser Ala Ala Phe Asp Gly
 1125 1130 1135

Ser Ile Lys Val Trp Glu Trp Gln Ser Lys
 1140 1145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATAAGAAGAT AGAAGATGAT ATTTAAAGTT TGGTTTTTCAT ATGAAGATGA GGAAGTGGAA	60
CTATCAGAAT TAACAAATGA TACAACAGTG TCAGCAATTA GAAAGATCTT ACATGAAGGT	120
AAAATATTTA GATTTCCATA TGGTACATCT CAAACAGACT TGCAAATTGG AAAGATGTTA	180
CCATCTGGTA GTGGTGGAGG TGCAACTGCA GACAGCAAAT TTGAGAAGTT TAAAGCACGT	240
AATACATTAG CAGATATTCA ATATAAAGTT GGTGATACAT TATATGTTAG AGTTAAAAAA	300
AGTAAACCAA CAAATGATTC ATTATTACCA ACATTAAATA TAGCATTTTT AGATGGATCA	360
GAACGTGCAA TTAAATGGGA ATATGACCCA TATACTACAA CTGCTCAATG GACCTGTACA	420
GCAACATTAG TCAAAGTTGA ACCAGTACCA TTTGCTGAAG GTGCATTTAG GAAAGCTTAT	480
CATACATTGG ATTTAAGTAA ATCTGGTGCA AGTGGAAGAT ATGTATCAAA GATTGGTAAA	540
AAACCAACAC CAAGACCATC ATATTTTGAA GATGTAAAGA TGCAAATGAT AGCAAAGAAA	600
TGGGCAGATA AATATAATTC ATTTAAACCT CAAAAAAGA TTGAATTTTT ACAATCATGC	660
GTTTTAGAGT TTGTAGATAG AACATCATCA GATTTAATTT GTGGAGCAGA ACCATATGTA	720
GAAGGACAAT ATAGAAAGTA TAATAATAAT AGTGGATTCG TTAGTAATGA TGAAAGAAAT	780
ACACCACAAT CATTCTCTCA TTTCACATAT GAACATTCAA ATCATCAATT ATTGATTATA	840
GATATTCAAG GTGTTGGTGA TCACTATACA GACCCACAAA TTCATACCTA TGATGGTGTT	900
GGTTTTGGTA TTGGTAATTT GGGTCAAAAA GTTTTTGAAA AGTTTTTTAGA TACTCATAAA	960
TGTAATGCAA TTTGCCAATA TTAAATTTA CAATCAATTA ATCCAAAATC TGAAAAAGT	1020
GATTGTGGTA CTGTACCAAG ACCAGATTTA ATTTCCCTG ATACATCTGA AAGAGATAAT	1080
AATAATAATA ATAATAATAA TAATAATAAT AATAATAATA ATAATAATAA TAATAGTAAT	1140
AATAATAATA ATAACAATAG TAGTATTTCA AAATCATTAG TTGAAATTTT AAGTGGTAGT	1200
AAAGAAAGAA ATGATAGAGA TTCGCCAAGT AGACAATTAT TTGTTTCAAA TGATGSTAAT	1260

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ACATTAAATA CAAATAAAGA GAGATCAAAA TCAAAATCAA TAGATTTAGA AAAACCAGAA	1320
ATTTTAATAA ATAATAAGAA AAAAGAGAGT ATAAATTTGG AAACGATAAA ATTAATTGAA	1380
ACTATTAAAG GATATCATGT TACAAGTCAT TTATGTATTT GTGATAATTT ATTATTTACA	1440
GGATGTTTCA ATAATTCAAT TAGAGTGTAT GATTATAAGA GTCAAAATAT GGAATGTGTT	1500
CAAACCTTGA AAGGTCATGA AGGTCCAGTT GAATCAATTT GTTATAATGA TCAATATTTG	1560
TTTAGTGGTT CATCAGATCA TTCAATTAAA GTTTGGGATT TAAAGAAATT AAGATGTATT	1620
TTTACTTTGG AGGGTCATGA TAAACCTGTC CATACGGTTC TATTGAATGA TAAATATTTG	1680
TTTAGTGGTT CCTCTGACAA AACTATCAAA GTTTGGGATT TGAAAACTTT GGAATGTAAA	1740
TATACCCTTG AAAGTCATGC CAGAGCCGTC AAAACACTTT GTATATCTGG TCAATATTTA	1800
TTTAGTGGTT CAAATGATAA AACTATCAAG GTTTGGGATT TGAAAACTTT TCGTTGTAAC	1860
TACACTCTAA AAGGTCATAC TAAATGGGTC ACCAATATCT GTATATTAGG TACCAATCTC	1920
TACAGTGGCT CCTATGATAA AACTATAAGA GTTTGGAATT TAAAGAGTTT AGAATGTTCC	1980
GCTACTTTAA GAGGCCATGA TAGATGGGTT GAACATATGG TAATTTGTGA TAAATTATTA	2040
TTTACTGCTA GTGACGATAA TACAATTAAA ATTTGGGATT TAGAAACATT AAGATGTAAT	2100
ACAACCTTGG AAGGACATAA TGCAACCGTT CAATGTTTAG CAGTTTGGGA AGATAAAAAA	2160
TGTGTTATTA GTTGTAGTCA TGATCAAAGT ATTAGAGTTT GGGGTTGGAA TTAATTTAAA	2220
ATAAAAAAAA AAAACAT	2237

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Dictyostelium discoideum

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Ile Phe Lys Val Trp Phe Ser Tyr Glu Asp Glu Glu Val Glu Leu
1           5           10           15

Ser Glu Leu Thr Asn Asp Thr Thr Val Ser Ala Ile Arg Lys Ile Leu
          20           25           30

His Glu Gly Lys Ile Phe Arg Phe Pro Tyr Gly Thr Ser Gln Thr Asp
          35           40           45

Leu Gln Ile Gly Lys Met Leu Pro Ser Gly Ser Gly Gly Gly Ala Thr
          50           55           60

Ala Asp Ser Lys Phe Glu Lys Phe Lys Ala Arg Asn Thr Leu Ala Asp
65           70           75           80

Ile Gln Tyr Lys Val Gly Asp Thr Leu Tyr Val Arg Val Lys Lys Ser
          85           90           95

Lys Pro Thr Asn Asp Ser Leu Leu Pro Thr Leu Asn Ile Ala Phe Leu
          100          105          110

Asp Gly Ser Glu Arg Ala Ile Lys Trp Glu Tyr Asp Pro Tyr Thr Thr
          115          120          125

Thr Ala Gln Trp Thr Cys Thr Ala Thr Leu Val Lys Val Glu Pro Val
          130          135          140

Pro Phe Ala Glu Gly Ala Phe Arg Lys Ala Tyr His Thr Leu Asp Leu
145          150          155          160

Ser Lys Ser Gly Ala Ser Gly Arg Tyr Val Ser Lys Ile Gly Lys Lys
          165          170          175

Pro Thr Pro Arg Pro Ser Tyr Phe Glu Asp Val Lys Met Gln Met Ile
          180          185          190

Ala Lys Lys Trp Ala Asp Lys Tyr Asn Ser Phe Lys Pro Pro Lys Lys
          195          200          205

Ile Glu Phe Leu Gln Ser Cys Val Leu Glu Phe Val Asp Arg Thr Ser
          210          215          220

Ser Asp Leu Ile Cys Gly Ala Glu Pro Tyr Val Glu Gly Gln Tyr Arg
225          230          235          240

Lys Tyr Asn Asn Asn Ser Gly Phe Val Ser Asn Asp Glu Arg Asn Thr
          245          250          255

Pro Gln Ser Phe Ser His Phe Thr Tyr Glu His Ser Asn His Gln Leu

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260	265	270
Leu Ile Ile Asp Ile Gln Gly Val Gly Asp His Tyr Thr Asp Pro Gln		
275	280	285
Ile His Thr Tyr Asp Gly Val Gly Phe Gly Ile Gly Asn Leu Gly Gln		
290	295	300
Lys Gly Phe Glu Lys Phe Leu Asp Thr His Lys Cys Asn Ala Ile Cys		
305	310	315
Gln Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp		
325	330	335
Cys Gly Thr Val Pro Arg Pro Asp Leu Ile Phe Pro Asp Thr Ser Glu		
340	345	350
Arg Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn		
355	360	365
Asn Asn Asn Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Ser Ser Ile		
370	375	380
Ser Lys Ser Leu Val Glu Ile Ser Ser Gly Ser Lys Glu Arg Asn Asp		
385	390	395
Arg Asp Ser Pro Ser Arg Gln Leu Phe Val Ser Asn Asp Gly Asn Thr		
405	410	415
Leu Asn Thr Asn Lys Glu Arg Ser Lys Ser Lys Ser Ile Asp Leu Glu		
420	425	430
Lys Pro Glu Ile Leu Ile Asn Asn Lys Lys Lys Glu Ser Ile Asn Leu		
435	440	445
Glu Thr Ile Lys Leu Ile Glu Thr Ile Lys Gly Tyr His Val Thr Ser		
450	455	460
His Leu Cys Ile Cys Asp Asn Leu Leu Phe Thr Gly Cys Ser Asp Asn		
465	470	475
Ser Ile Arg Val Tyr Asp Tyr Lys Ser Gln Asn Met Glu Cys Val Gln		
485	490	495
Thr Leu Lys Gly His Glu Gly Pro Val Glu Ser Ile Cys Tyr Asn Asp		
500	505	510
Gln Tyr Leu Phe Ser Gly Ser Ser Asp His Ser Ile Lys Val Trp Asp		
515	520	525
Leu Lys Lys Leu Arg Cys Ile Phe Thr Leu Glu Gly His Asp Lys Pro		

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530	535	540
Val His Thr Val Leu Leu Asn Asp Lys Tyr Leu Phe Ser Gly Ser Ser		
545	550	555 560
Asp Lys Thr Ile Lys Val Trp Asp Leu Lys Thr Leu Glu Cys Lys Tyr		
	565	570 575
Thr Leu Glu Ser His Ala Arg Ala Val Lys Thr Leu Cys Ile Ser Gly		
	580	585 590
Gln Tyr Leu Phe Ser Gly Ser Asn Asp Lys Thr Ile Lys Val Trp Asp		
	595	600 605
Leu Lys Thr Phe Arg Cys Asn Tyr Thr Leu Lys Gly His Thr Lys Trp		
	610	615 620
Val Thr Thr Ile Cys Ile Leu Gly Thr Asn Leu Tyr Ser Gly Ser Tyr		
	625	630 635 640
Asp Lys Thr Ile Arg Val Trp Asn Leu Lys Ser Leu Glu Cys Ser Ala		
	645	650 655
Thr Leu Arg Gly His Asp Arg Trp Val Glu His Met Val Ile Cys Asp		
	660	665 670
Lys Leu Leu Phe Thr Ala Ser Asp Asp Asn Thr Ile Lys Ile Trp Asp		
	675	680 685
Leu Glu Thr Leu Arg Cys Asn Thr Thr Leu Glu Gly His Asn Ala Thr		
	690	695 700
Val Gln Cys Leu Ala Val Trp Glu Asp Lys Lys Cys Val Ile Ser Cys		
	705	710 715 720
Ser His Asp Gln Ser Ile Arg Val Trp Gly Trp Asn		
	725	730

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACGATCG ACACAACAAA TGAGAGCGAC AATAGTCCAA CTAAGTCACC AGGATTGGAG	60
GCCTCGGCTC GGACATTCTC GGTCAATGCG TCAAAAATGG TTCGGATAAC CGACGACTAC	120
GCAGATGAAG TGTTCATTGA ACAGAATGAT GTCGTTATCG AGAAGCCTCG TATGGATCCT	180
CTCCACGTTA GAAAACTTAT GGAGACATGG CGCAAGGCTG CTCGCCGAGC AAGAACAAAC	240
TATATAGATC CATGGGATGA GTTCAACATC CACGAGTATC CAGTACAACG AGCTAAACGA	300
TATAGGTATT CTGCAATCAG AAAGCAATGG ACAGAGGATA TAGTCGATGT GAGACTTCAT	360
CCGGACAGTT TTGCAGGTGG AGGCATGCGA GAATGCTACC GACTCAAAAA GTGCTCCAAG	420
CACGSAACAA GTCAAGATTG GAGCAGCAAC TATGTGCGAA AAAGATACAT TTGTCAAGTC	480
GATCGTAGAG TTCTTTTCGA TGATGTCAGA CTTCAGATGG ATGCCAAATT ATGGGCTGAA	540
GAATATAATC GGTATAATCC ACCGAAGAAA ATTGATATTG TTCAAATGTG TGTCATTGAG	600
ATGATTGATG TAAAAGGTTT TCCACTCTAT CATTTGGAGC ATTTTCATCGA GGGAAAATAT	660
ATAAAATACA ATTCAAATC AGGATTTGTA TCAAATGCAG CTCGTCTTAC ACCACAAGCA	720
TTTTCTCACT TCACCTTCGA AGTTCTGGT CATCAAATGA TGTTGTGCGA TATTCAAGGA	780
GTTGGTGATC TTTACACAGA TCCTCAGATT CATAAGTTG TGGGAAGTGA TTATGGAGAT	840
GGAAACCTCG GAACTCGTGG AATGGCTCTT TTCTTCCATT CACACAGATG TAACGATATT	900
TGTGAGACAA TGGATCTATC AAATTTGGA CTTTCGCCAC CTGAAATCGA GGCTACCGAA	960
GTTGCGATGG AAGTAGCTGC AAAGCAGAAA AAGTCATGCA TAGTTCCTCC AACTGTGTTC	1020
GAAGCAAGAA GAAATCGAAT TTCAAGTGAA TGTGTACATG TCGAGCATGG TATTTGATG	1080
GATCAATTGA GAAAAAGGAA GACGTTGAAT CAATCGTCAA CCGATTGTGC AGCAAAGAGT	1140
CACAACGAAG ACTGTGTATG TCCTGAGTGT ATTCCAGTTG TTGAGCAACT CTGTGAGCCT	1200
TGCTCCGAAG ATGAAGAGGA CGAAGAAGAA GACTATCCAA GAAGTGAAAA AAGTGGAAT	1260
AGTCAGAAAA GTCGACGTAG TAGAATGAGC ATTTCAACGA GATCTTCTGG CGATGAATCA	1320
GCATCTCGTC CTAGAAAATG CGGATTTGTA GATTTAAAT CACTTCGTCA GAGACATGAT	1380

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AGCTTCAGAA GTTCTGTTGG GACATATTCT ATGAATAGTT CTAGACAAAC CAGAGACACT 1440
GAAAAGGATG AATTCTGGAA GGTCTTCGA AAACAATCAG TTCCAGCAAA CATTCTATCA 1500
CTTCAACTTC AACAAATGGC TGCTAACCTG GAAAATGATG AAGACGTACC ACAAGTCACC 1560
GGGCATCAGT TCTCTGTCTT CGGTCAGATT CATATTGATC TCTCAGATA TCATGAGCTC 1620
GGGCGGTTTC TAGAAGTTGA TTCAGAACAT AAGGAAATGC TTGAGGGAAG TGAAAATGAC 1680
GCTCGTGTAC CAATCAAATA CGACAAGCAG TCTGCAATTT TCCATTTGGA TATCGCTCGG 1740
AAGTGTGGAA TCCTTGAGGC TGTGCTAACA TCGGCTCATA TTGTTCTCGG ATTACCACAT 1800
GAATTGTTGA AAGAAGTCAC CGTTGATGAT CTGTTTCCTA ATGGGTTTGG AGAACAGGAA 1860
AATGGAATTC GAGCTGATAA AGGACAAAAA CCTTGTGACC TAGAAGAGTT CGGCTCCGAT 1920
CTGATGGAAA TTGCTGCAGA GATGGGTGAT AAGGSTGCAA TGCTGTACAT GGCACACGCT 1980
TATGAAACTG GTCAGCATCT CGSACCGAAT CGAAGAACGG ATTATAAGAA ATCGATTGAT 2040
TGGTATCAAC GCGTCGTTGG ATTCCAAGAA GAAGAAGAAC TTGACTCTGA TTGTGGAAAA 2100
ACGACATTCT CCTCATTTGC TCCACTGACT CGTCACGAGA TTCTAGCCAA AATGGCTGAA 2160
ATGTACAAAG AGGGAGGTTA TGGCCTGAAT CAAGACTTCG AACGAGCATA TGGTCTATTC 2220
AATGAAGCTG CTGAAGCAGC AATGGAAGCA ATGAATGGAA AGCTCGCAA TAAATACTAT 2280
GAAAAAGCGG AAATGTGTGG AGAATGA 2307

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
 1 5 10 15
 Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
 20 25 30
 Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
 35 40 45
 Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
 50 55 60
 Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
 65 70 75 80
 Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
 85 90 95
 Arg Ala Lys Arg Tyr Arg Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
 100 105 110
 Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
 115 120 125
 Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
 130 135 140
 Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
 145 150 155 160
 Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys
 165 170 175
 Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp
 180 185 190
 Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro
 195 200 205
 Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
 210 215 220
 Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala
 225 230 235 240
 Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Met Met Val Val
 245 250 255
 Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr
 260 265 270

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Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu Gly Thr Arg Gly Met
275 280 285

Ala Leu Phe Phe His Ser His Arg Cys Asn Asp Ile Cys Glu Thr Met
290 295 300

Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu Ile Glu Ala Thr Glu
305 310 315 320

Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys Ser Cys Ile Val Pro
325 330 335

Pro Thr Val Phe Glu Ala Arg Arg Asn Arg Ile Ser Ser Glu Cys Val
340 345 350

His Val Glu His Gly Ile Ser Met Asp Gln Leu Arg Lys Arg Lys Thr
355 360 365

Leu Asn Gln Ser Ser Thr Asp Leu Ser Ala Lys Ser His Asn Glu Asp
370 375 380

Cys Val Cys Pro Glu Cys Ile Pro Val Val Glu Gln Leu Cys Glu Pro
385 390 395 400

Cys Ser Glu Asp Glu Glu Asp Glu Glu Glu Asp Tyr Pro Arg Ser Glu
405 410 415

Lys Ser Gly Asn Ser Gln Lys Ser Arg Arg Ser Arg Met Ser Ile Ser
420 425 430

Thr Arg Ser Ser Gly Asp Glu Ser Ala Ser Arg Pro Arg Lys Cys Gly
435 440 445

Phe Val Asp Leu Asn Ser Leu Arg Gln Arg His Asp Ser Phe Arg Ser
450 455 460

Ser Val Gly Thr Tyr Ser Met Asn Ser Ser Arg Gln Thr Arg Asp Thr
465 470 475 480

Glu Lys Asp Glu Phe Trp Lys Val Leu Arg Lys Gln Ser Val Pro Ala
485 490 495

Asn Ile Leu Ser Leu Gln Leu Gln Gln Met Ala Ala Asn Leu Glu Asn
500 505 510

Asp Glu Asp Val Pro Gln Val Thr Gly His Gln Phe Ser Val Leu Gly
515 520 525

Gln Ile His Ile Asp Leu Ser Arg Tyr His Glu Leu Gly Arg Phe Val
530 535 540

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Glu Val Asp Ser Glu His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp			
545	550	555	560
Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu			
	565	570	575
Asp Ile Ala Arg Lys Cys Gly Ile Leu Glu Ala Val Leu Thr Ser Ala			
	580	585	590
His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val			
	595	600	605
Asp Asp Leu Phe Pro Asn Gly Phe Gly Glu Gln Glu Asn Gly Ile Arg			
	610	615	620
Ala Asp Lys Gly Gln Lys Pro Cys Asp Leu Glu Glu Phe Gly Ser Asp			
	625	630	635
Leu Met Glu Ile Ala Ala Glu Met Gly Asp Lys Gly Ala Met Leu Tyr			
	645	650	655
Met Ala His Ala Tyr Glu Thr Gly Gln His Leu Gly Pro Asn Arg Arg			
	660	665	670
Thr Asp Tyr Lys Lys Ser Ile Asp Trp Tyr Gln Arg Val Val Gly Phe			
	675	680	685
Gln Glu Glu Glu Glu Leu Asp Ser Asp Cys Gly Lys Thr Thr Phe Ser			
	690	695	700
Ser Phe Ala Pro Leu Thr Arg His Glu Ile Leu Ala Lys Met Ala Glu			
	705	710	715
Met Tyr Lys Glu Gly Gly Tyr Gly Leu Asn Gln Asp Phe Glu Arg Ala			
	725	730	735
Tyr Gly Leu Phe Asn Glu Ala Ala Glu Ala Ala Met Glu Ala Met Asn			
	740	745	750
Gly Lys Leu Ala Asn Lys Tyr Tyr Glu Lys Ala Glu Met Cys Gly Glu			
	755	760	765

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGACGATCG ACACAACAAA TGAGAGCGAC AATAGTCCAA CTAAGTCACC AGGATTGGAG	60
GCCTCGGCTC GSACATTCTC GGTCAATGCG TCAAAAATGG TTCGGATAAC CGACGACTAC	120
GCAGATGAAG TGTTTCATTGA ACAGAATGAT GTCGTTATCG AGAAGCCTCG TATGGATCCT	180
CTCCACGTTA GAAAACTTAT GGAGACATGG CGCAAGGCTG CTCGCCGAGC AAGAACAAAC	240
TATATAGATC CATGGGATGA GTTCAACATC CACGAGTATC CAGTACAACG AGCTAAACGA	300
TATAGGTATT CTGCAATCAG AAAGCAATGG ACAGAGGATA TAGTCGATGT GAGACTTCAT	360
CCGGACAGTT TTGCACGTGG AGCCATGCGA GAATGCTACC GACTCAAAAA GTGCTCCAAG	420
CACGGAACAA GTCAAGATTG GAGCAGCAAC TATGTGCGAA AAAGATACAT TTGTCAAGTC	480
GATCGTAGAG TTCTTTTCGA TGATGTCAGA CTTGAGATGG ATGCCAAATT ATGGGCTGAA	540
GAATATAATC GGTATAATCC ACCGAAGAAA ATTGATATTG TTCAAATGTG TGTCATTGAG	600
ATGATTGATG TAAAAGGTTC TCCACTCTAT CATTGAGAGC ATTTTCATCGA GGGAAAATAT	660
ATAAAATACA ATTCAAATC AGGATTTGTA TCAAATGCAG CTCGTCTTAC ACCACAAGCA	720
TTTTCTCACT TCACCTTCGA ACGTTCTGGT CATCAAATGA TGGTTGTCGA TATTCAAGGA	780
GTTGGTGATC TTTACACAGA TCCTCAGATT CATAAGTTG TGGGAACTGA TTATGGAGAT	840
GGAAACCTCG GAACTCGTGG AATGGCTCTT TTCTTCCATT CACACAGATG TAACGATATT	900
TGTGAGACAA TGGATCTATC AAATTTTCGAA CTTTCGCCAC CTGAAATCGA GGCTACCGAA	960
GTTGCGATGG AAGTAGCTGC AAAGCAGAAA AAGTCATGCA TAGTTCCTCC AACTGTGTTC	1020
GAAGCAAGAA GAAATCGAAT TTCAAGTGAA TGTGTACATG TCGAGCATGG TATTTTCGATG	1080
GATCAATTGA GAAAAAGGAA GACGTTGAAT CAATCGTCAA CCGATTTGTC AGCAAAGAGT	1140
CACAACGAAG ACTGTGTATG TCCTGAGTGT ATTCCAGTTG TTGAGCAACT CTGTGAGCCT	1200

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TGCTCCGAAG ATGAAGAGGA CGAAGAAGAA GACTATCCAA GAAGTGAAAA AAGTGGAAT 1260
AGTCAGAAAA GTCGACGTAG TAGAATGAGC ATTTCAACGA GATCTTCTGG CGATGAATCA 1320
GCATCTCGTC CTAGAAAATG CGGATTTGTA GATTTAACT CACTTCGTCA GAGACATGAT 1380
AGCTTCAGAA GTTCTGTTGG GACATATTCT ATGAATAGTT CTAGACAAAC CAGAGACACT 1440
GAAAAGGATG AATTCTGGAA GGTTCCTCGA AAACAATCAG TTCCAGCAA CATTCTATCA 1500
CTTCAACTTC AACAAATGSC TGCTAACCTG GAAATGATG AAGACGTACC ACAAGTCACC 1560
GGGCATCAGT TCTCTGTCCT CGGTCAGATT CATATTGATC TCTCAGATA TCATGAGCTC 1620
GGGCGGTTCC TAGAAGTTGA TTCAGAACAT AAGGAAATGC TTGAGGGAAG TGAAAATGAC 1680
GCTCGTGTA CAATCAAATA CGACAAGCAG TCTGCAATTT TCCATTTGGA TATCGCTCGG 1740
AAGTGTGSAA TCCTTGAGGC TGTGCTAACA TCGGCTCATA TTGTTCTCGG ATTACCACAT 1800
GAATTGTTGA AAGAAETCAC CTTGATGAT CTGTTTCCTA ATGGGTTTGG AGAACAGGAA 1860
AATGGAATTC GAGACCTAGA AGAGTTCGGC TCCGATCTGA TGSAAATTGC TGCAGAGATG 1920
GGTGATAAGG GTGCAATGCT GTACATGGCA CACGCTTATG AAAGTGGTCA GCATCTCGGA 1980
CCGAATCGAA GAACGGATTA TAAGAAATCG ATTGATTGGT ATCAACGCGT CGTTGGATTC 2040
CAAGAAGAA AAGAACTTGA CTCTGATTGT GGAAAAACGA CATTCTCCTC ATTTGCTCCA 2100
CTGACTCGTC ACGAGATTCT AGCCAAAATG GCTGAAATGT ACAAAGAGGG AGGTTATGGC 2160
CTGAATCAAG ACTTCGAACG ASCATATGGT CTATTCAATG AAGCTGCTGA AGCAGCAATG 2220
GAAGCAATGA ATGGAAAGCT CGCAAATAAA TACTATGAAA AAGCGGAAAT GTGTGGAGAA 2280
TGA 2283

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
1           5           10           15

Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
20           25           30

Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
35           40           45

Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
50           55           60

Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
65           70           75           80

Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
85           90           95

Arg Ala Lys Arg Tyr Arg Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
100          105          110

Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
115          120          125

Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
130          135          140

Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
145          150          155          160

Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys
165          170          175

Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp
180          185          190

Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro
195          200          205

Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
210          215          220

Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala
225          230          235          240

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Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	Gln	Met	Met	Val	Val		
				245					250				255				
Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp	Pro	Gln	Ile	His	Thr		
				260					265				270				
Val	Val	Gly	Thr	Asp	Tyr	Gly	Asp	Gly	Asn	Leu	Gly	Thr	Arg	Gly	Met		
				275					280				285				
Ala	Leu	Phe	Phe	His	Ser	His	Arg	Cys	Asn	Asp	Ile	Cys	Glu	Thr	Met		
				290					295				300				
Asp	Leu	Ser	Asn	Phe	Glu	Leu	Ser	Pro	Pro	Glu	Ile	Glu	Ala	Thr	Glu		
305					310					315				320			
Val	Ala	Met	Glu	Val	Ala	Ala	Lys	Gln	Lys	Lys	Ser	Cys	Ile	Val	Pro		
				325					330				335				
Pro	Thr	Val	Phe	Glu	Ala	Arg	Arg	Asn	Arg	Ile	Ser	Ser	Glu	Cys	Val		
				340					345				350				
His	Val	Glu	His	Gly	Ile	Ser	Met	Asp	Gln	Leu	Arg	Lys	Arg	Lys	Thr		
				355					360				365				
Leu	Asn	Gln	Ser	Ser	Thr	Asp	Leu	Ser	Ala	Lys	Ser	His	Asn	Glu	Asp		
				370					375				380				
Cys	Val	Cys	Pro	Glu	Cys	Ile	Pro	Val	Val	Glu	Gln	Leu	Cys	Glu	Pro		
385					390					395				400			
Cys	Ser	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Tyr	Pro	Arg	Ser	Glu		
				405					410				415				
Lys	Ser	Gly	Asn	Ser	Gln	Lys	Ser	Arg	Arg	Ser	Arg	Met	Ser	Ile	Ser		
				420					425				430				
Thr	Arg	Ser	Ser	Gly	Asp	Glu	Ser	Ala	Ser	Arg	Pro	Arg	Lys	Cys	Gly		
				435					440				445				
Phe	Val	Asp	Leu	Asn	Ser	Leu	Arg	Gln	Arg	His	Asp	Ser	Phe	Arg	Ser		
				450					455				460				
Ser	Val	Gly	Thr	Tyr	Ser	Met	Asn	Ser	Ser	Arg	Gln	Thr	Arg	Asp	Thr		
465					470					475				480			
Glu	Lys	Asp	Glu	Phe	Trp	Lys	Val	Leu	Arg	Lys	Gln	Ser	Val	Pro	Ala		
				485					490				495				
Asn	Ile	Leu	Ser	Leu	Gln	Leu	Gln	Gln	Met	Ala	Ala	Asn	Leu	Glu	Asn		
				500					505				510				

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Asp Glu Asp Val Pro Gln Val Thr Gly His Gln Phe Ser Val Leu Gly
 515 520 525
 Gln Ile His Ile Asp Leu Ser Arg Tyr His Glu Leu Gly Arg Phe Val
 530 535 540
 Glu Val Asp Ser Glu His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp
 545 550 555 560
 Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu
 565 570 575
 Asp Ile Ala Arg Lys Cys Gly Ile Leu Glu Ala Val Leu Thr Ser Ala
 580 585 590
 His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val
 595 600 605
 Asp Asp Leu Phe Pro Asn Gly Phe Gly Glu Gln Glu Asn Gly Ile Arg
 610 615 620
 Asp Leu Glu Glu Phe Gly Ser Asp Leu Met Glu Ile Ala Ala Glu Met
 625 630 635 640
 Gly Asp Lys Gly Ala Met Leu Tyr Met Ala His Ala Tyr Glu Thr Gly
 645 650 655
 Gln His Leu Gly Pro Asn Arg Arg Thr Asp Tyr Lys Lys Ser Ile Asp
 660 665 670
 Trp Tyr Gln Arg Val Val Gly Phe Gln Glu Glu Glu Glu Leu Asp Ser
 675 680 685
 Asp Cys Gly Lys Thr Thr Phe Ser Ser Phe Ala Pro Leu Thr Arg His
 690 695 700
 Glu Ile Leu Ala Lys Met Ala Glu Met Tyr Lys Glu Gly Gly Tyr Gly
 705 710 715 720
 Leu Asn Gln Asp Phe Glu Arg Ala Tyr Gly Leu Phe Asn Glu Ala Ala
 725 730 735
 Glu Ala Ala Met Glu Ala Met Asn Gly Lys Leu Ala Asn Lys Tyr Tyr
 740 745 750
 Glu Lys Ala Glu Met Cys Gly Glu
 755 760

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTATTGTATG TGTTC AATT GAGAAGACTC CATTTCGAAA GGGTAGTTGT AGAACAGCAC	60
ATAAATTAAA GGATTGGAGT CAACCAGATC AAGGATTAGT TGGTAAATTT TCAACCAATA	120
AAAAGACGAC AAGAGATTCA TACTTTACAG ATGTATTGAT GCAAACATTT TGTGCTAAAT	180
GGGCAGAGAA ATTCAATGAA GCGAAACCAC CAAAACCAAT TACATTCTTA CCATCATACG	240
TTTACGAATT GATTGATCAT CCACCACCTT ATCCAGTTTG TGGTGGTGAA CCATTCATTG	300
AGGGAGATTA CAAGAAACAT AACAACAACA GTGGTTACGT TAGTAGTGAT GCTAGAAATA	360
CACCACAATC ATTCTCTCAT TTCTCATACG AACTCTCCAA TCATGAATTG TTGATCGTTG	420
ATATCCAAGG TGTCAACGAT TTCTACACTG ATCCTCAAAT TCATACGAAA TCAGGCGAGG	480
GCTTTGGCGA GGGTAATTTG GCGGAGACGG GTTTCACAA ATTCTTCAA ACACACAAGT	540
GTAATCCAGT TTGTGACTTT TTAAAGTTGA AACCAATCAA TCAATCAAAG AAAGCCCTCC	600
TAAGAGGTAC ATTACCCGTC GTACAATT	628

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

-35-

(A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Ile Val Cys Val Ser Ile Glu Lys Thr Pro Phe Ala Lys Gly Ser Cys
1           5           10           15

Arg Thr Ala His Lys Leu Lys Asp Trp Ser Gln Pro Asp Gln Gly Leu
20           25           30

Val Gly Lys Phe Ser Thr Asn Lys Lys Thr Thr Arg Asp Ser Tyr Phe
35           40           45

Thr Asp Val Leu Met Gln Thr Phe Cys Ala Lys Trp Ala Glu Lys Phe
50           55           60

Asn Glu Ala Lys Pro Pro Lys Pro Ile Thr Phe Leu Pro Ser Tyr Val
65           70           75           80

Tyr Glu Leu Ile Asp His Pro Pro Pro Tyr Pro Val Cys Gly Gly Glu
85           90           95

Pro Phe Ile Glu Gly Asp Tyr Lys Lys His Asn Asn Asn Ser Gly Tyr
100          105          110

Val Ser Ser Asp Ala Arg Asn Thr Pro Gln Ser Phe Ser His Phe Ser
115          120          125

Tyr Glu Leu Ser Asn His Glu Leu Leu Ile Val Asp Ile Gln Gly Val
130          135          140

Asn Asp Phe Tyr Thr Asp Pro Gln Ile His Thr Lys Ser Gly Glu Gly
145          150          155          160

Phe Gly Glu Gly Asn Leu Gly Glu Thr Gly Phe His Lys Phe Leu Gln
165          170          175

Thr His Lys Cys Asn Pro Val Cys Asp Phe Leu Lys Leu Lys Pro Ile
180          185          190

Asn Gln Ser Lys Lys Ala Leu Leu Arg Gly Thr Leu Pro Val Val Gln
195          200          205

Leu

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

-36-

(A) LENGTH: 238 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly	Glu	Trp	Leu	Asp	Asp	Glu	Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	1	5	10	15
Phe	Gly	Arg	Gly	Ala	Met	Arg	Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	20	25	30	
Asn	Phe	Leu	His	Ala	Gln	Gln	Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	35	40	45	
Lys	Arg	Tyr	Ile	Glu	Pro	Val	Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	50	55	60	
Arg	Leu	Gln	Met	Glu	Ala	Lys	Leu	Trp	Gly	Glu	Glu	Tyr	Asn	Arg	His	65	70	75	80
Lys	Pro	Pro	Lys	Gln	Val	Asp	Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	85	90	95	
Lys	Asp	Arg	Pro	Gly	Lys	Pro	Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	100	105	110	
Gly	Lys	Tyr	Ile	Lys	Tyr	Asn	Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	115	120	125	
Asn	Ile	Arg	Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	130	135	140	
Ser	Gly	His	Gln	Leu	Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	145	150	155	160
Tyr	Thr	Asp	Pro	Gln	Ile	His	Thr	Glu	Thr	Gly	Thr	Asp	Phe	Gly	Asp	165	170	175	
Gly	Asn	Leu	Gly	Val	Arg	Gly	Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	180	185	190	

-37-

Cys Asn Arg Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser
 195 200 205

Pro Arg Glu Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser
 210 215 220

Ala Lys Thr Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser
 225 230 235

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: D. discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Lys Trp Ile Arg Leu Ser Met Lys Leu Lys Val Glu Arg Lys Pro
 1 5 10 15

Phe Ala Glu Gly Ala Leu Arg Glu Ala Tyr His Thr Val Ser Leu Gly
 20 25 30

Val Gly Thr Asp Glu Asn Tyr Pro Leu Gly Thr Thr Thr Lys Leu Phe
 35 40 45

Pro Pro Ile Glu Met Ile Ser Pro Ile Ser Lys Asn Asn Glu Ala Met
 50 55 60

Thr Gln Leu Lys Asn Gly Thr Lys Phe Val Leu Lys Leu Tyr Lys Lys
 65 70 75 80

Glu Ala Glu Gln Gln Ala Ser Arg Glu Leu Tyr Phe Glu Asp Val Lys
 85 90 95

Met Gln Met Val Cys Arg Asp Trp Gly Asn Lys Phe Asn Gln Lys Lys
 100 105 110

Pro Pro Lys Lys Ile Glu Phe Leu Met Ser Trp Val Val Glu Leu Ile
 115 120 125

-38-

```

Asp Arg Ser Pro Ser Ser Asn Gly Gln Pro Ile Leu Cys Ser Ile Glu
 130                      135                      140

Pro Leu Leu Val Gly Glu Phe Lys Lys Asn Asn Ser Asn Tyr Gly Ala
 145                      150                      155                      160

Val Leu Thr Asn Arg Ser Thr Pro Gln Ala Phe Ser His Phe Thr Tyr
                      165                      170                      175

Glu Leu Ser Asn Lys Gln Met Ile Val Val Asp Ile Gln Gly Val Asp
                      180                      185                      190

Asp Leu Tyr Thr Asp Pro Gln Ile His Thr Pro Asp Gly Lys Gly Phe
 195                      200                      205

Gly Leu Gly Asn Leu Gly Lys Ala Gly Ile Asn Lys Phe Ile Thr Thr
 210                      215                      220

His Lys Cys Asn Ala Val Cys Ala Leu Leu Asp Leu Asp Val Lys Leu
 225                      230                      235                      240

Gly Gly Val Leu Ser Gly Asn Asn Lys Lys Gln Leu Gln Gln Gly Thr
                      245                      250                      255

Met Val

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: D. discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Ala Gln Trp Thr Cys Thr Ala Thr Leu Val Lys Val Glu Pro Val Pro
 1                      5                      10                      15

Phe Ala Glu Gly Ala Phe Arg Lys Ala Tyr His Thr Leu Asp Leu Ser
                      20                      25                      30

```

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Lys Ser Gly Ala Ser Gly Arg Tyr Val Ser Lys Ile Gly Lys Lys Pro
 35 40 45
 Thr Pro Arg Pro Ser Tyr Phe Glu Asp Val Lys Met Gln Met Ile Ala
 50 55 60
 Lys Lys Trp Ala Asp Lys Tyr Asn Ser Phe Lys Pro Pro Lys Lys Ile
 65 70 75 80
 Glu Phe Leu Gln Ser Cys Val Leu Glu Phe Val Asp Arg Thr Ser Ser
 85 90 95
 Asp Leu Ile Cys Gly Ala Glu Pro Tyr Val Glu Gly Gln Tyr Arg Lys
 100 105 110
 Tyr Asn Asn Asn Ser Gly Phe Val Ser Asn Asp Glu Arg Asn Thr Pro
 115 120 125
 Gln Ser Phe Ser His Phe Thr Tyr Glu His Ser Asn His Gln Leu Leu
 130 135 140
 Ile Ile Asp Ile Gln Gly Val Gly Asp His Tyr Thr Asp Pro Gln Ile
 145 150 155 160
 His Thr Tyr Asp Gly Val Gly Phe Gly Ile Gly Asn Leu Gly Gln Lys
 165 170 175
 Gly Phe Glu Lys Phe Leu Asp Thr His Lys Cys Asn Ala Ile Cys Gln
 180 185 190
 Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp Cys
 195 200 205
 Gly Thr Val Pro
 210

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: C. elegans

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Gln Trp Thr Glu Asp Ile Val Asp Val Arg Leu His Pro Asp Ser
 1 5 10 15
 Phe Ala Arg Gly Ala Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser
 20 25 30
 Lys His Gly Thr Ser Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg
 35 40 45
 Tyr Ile Cys Gln Val Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu
 50 55 60
 Gln Met Asp Ala Lys Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro
 65 70 75 80
 Pro Lys Lys Ile Asp Ile Val Gln Met Cys Val Ile Glu Met Ile Asp
 85 90 95
 Val Lys Gly Ser Pro Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys
 100 105 110
 Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg
 115 120 125
 Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His
 130 135 140
 Gln Met Met Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
 145 150 155 160
 Pro Gln Ile His Thr Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu
 165 170 175
 Gly Thr Arg Gly Met Ala Leu Phe Phe His Ser His Arg Cys Asn Asp
 180 185 190
 Ile Cys Glu Thr Met Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu
 195 200 205
 Ile Glu Ala Thr Glu Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys
 210 215 220
 Ser Cys Ile Val Pro Pro Thr Val Phe
 225 230

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

-41-

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide Primer D"

(iii) HYPOTHETICAL: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATTTGGAC TGGACAAGAA CCCCC

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg	Lys	Lys	Phe	Gly	Glu	Ser	Glu	Lys	Thr	Lys	Thr	Lys	Glu	Phe	Leu
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

-42-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Ala Asn Xaa Tyr Tyr Glu Lys Ala Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGCCTTNN NNCANTTNAC NTTNGANNG

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

-43-

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCNGCNTTNT CNTANTANTT NTTNGC

26

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACAATCAGC TGATGACCAG AACGCTC

27



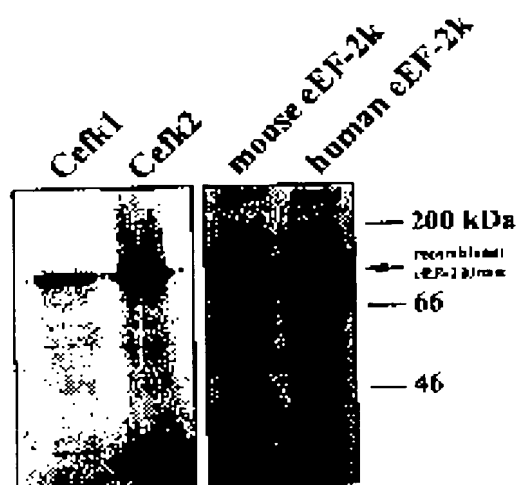


FIGURE 2

SUBSTITUTE SHEET (RULE 26)

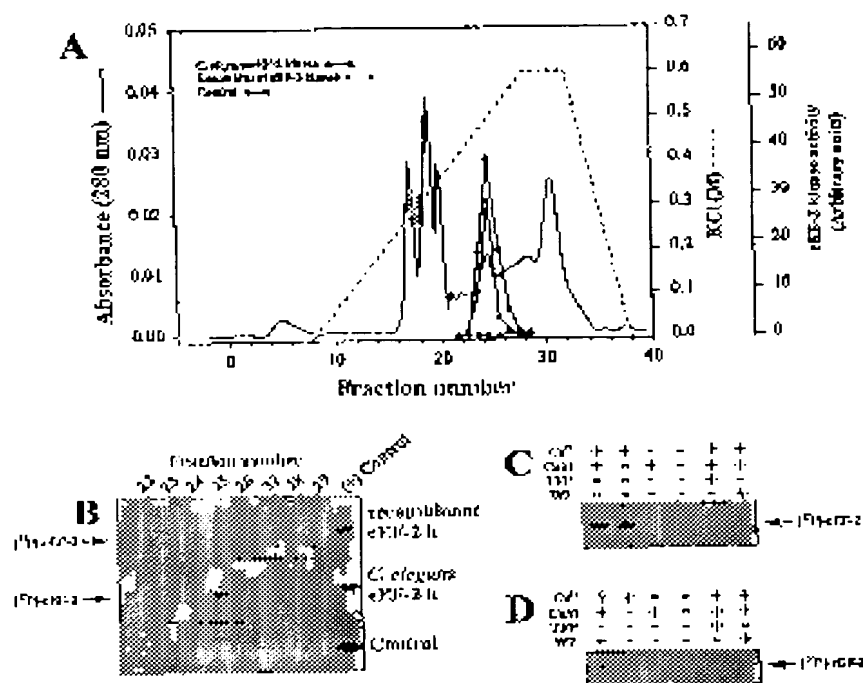


FIGURE 3

SUBSTITUTE SHEET (RULE 26)

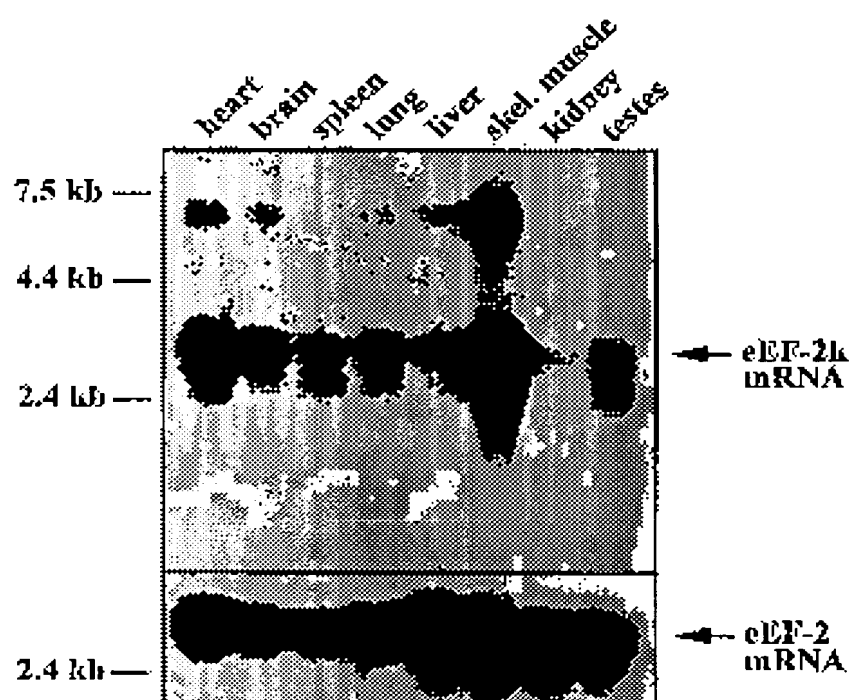


FIGURE 4

SUBSTITUTE SHEET (RULE 26)

[illegible]

FIGURE 5

SUBSTITUTE SHEET (RULE 26)

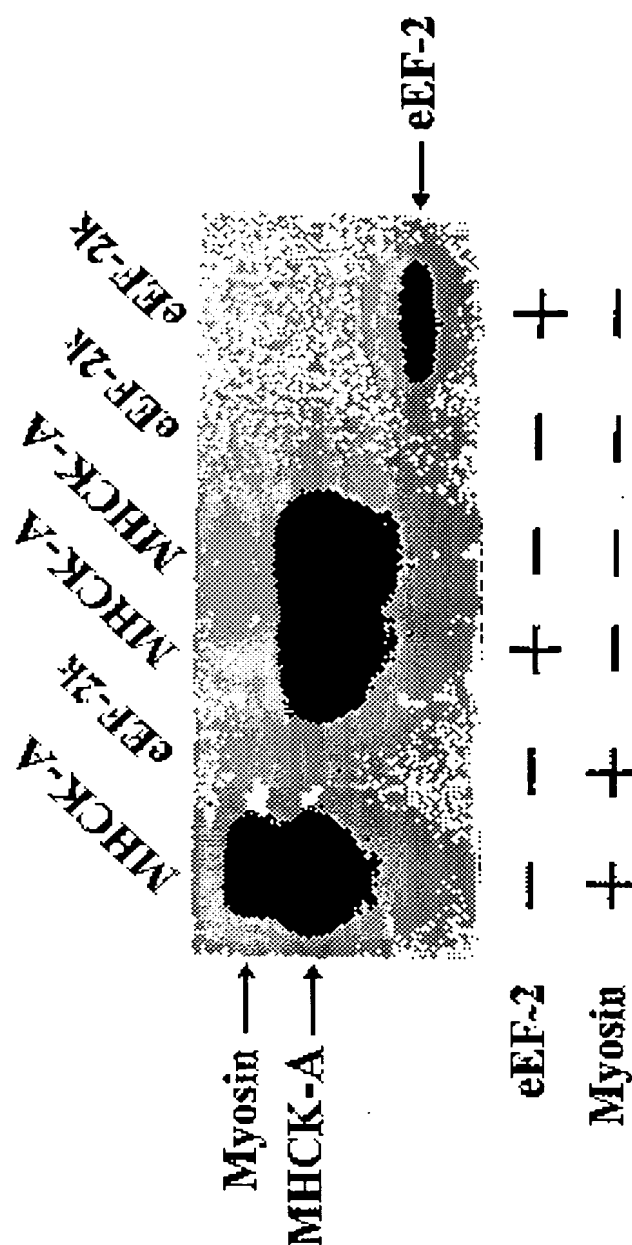


FIGURE 6

SUBSTITUTE SHEET (RULE 26)

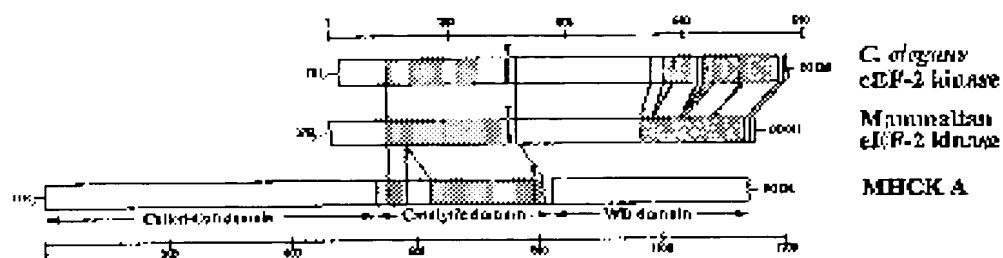


FIGURE 7

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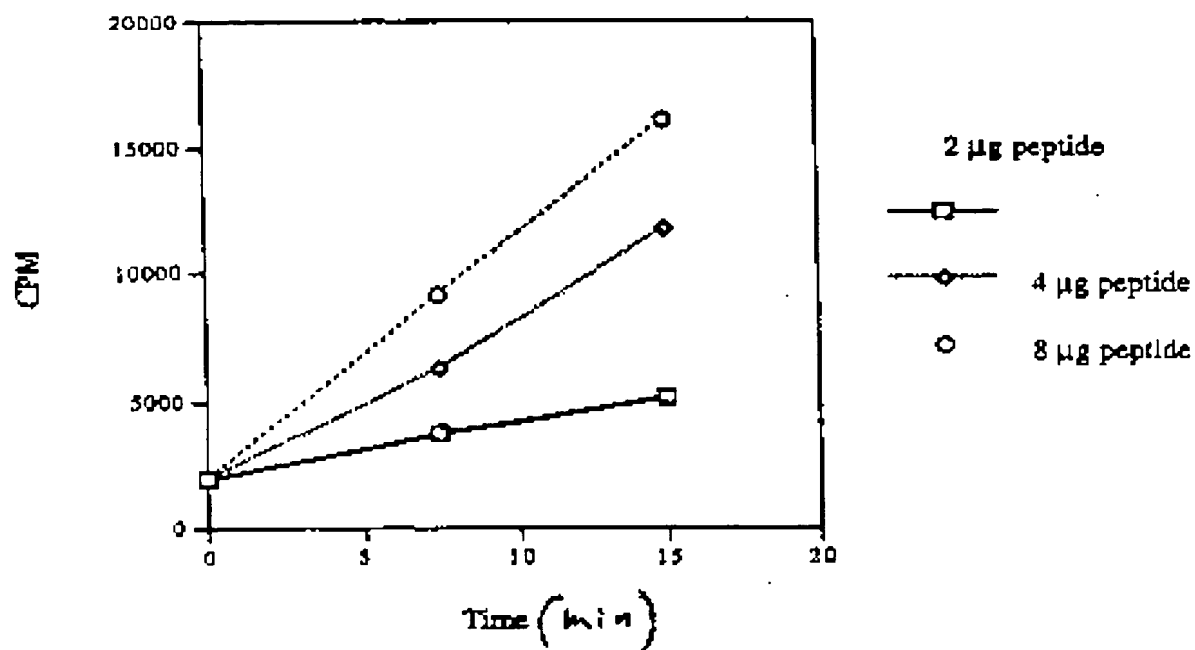


FIGURE 8

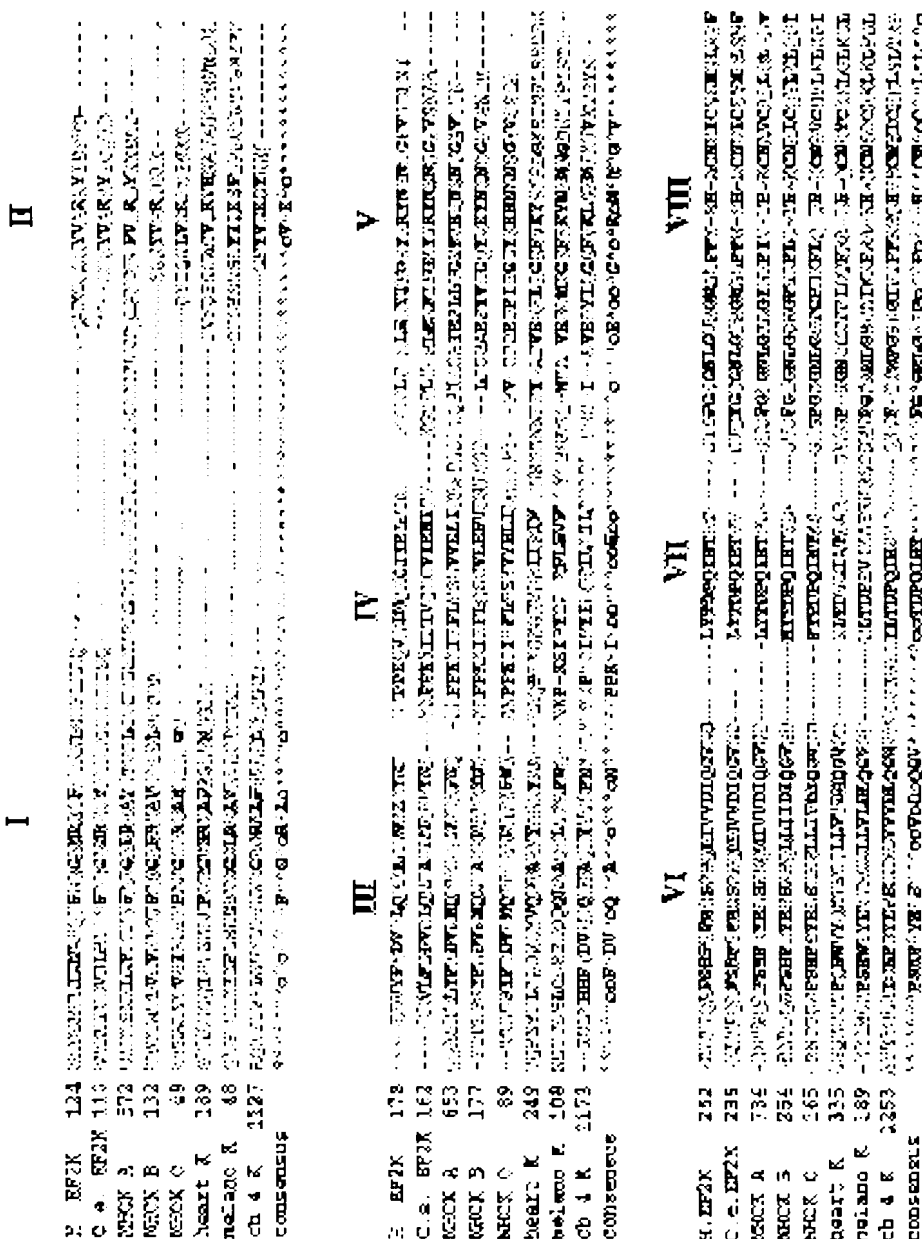


FIGURE 9

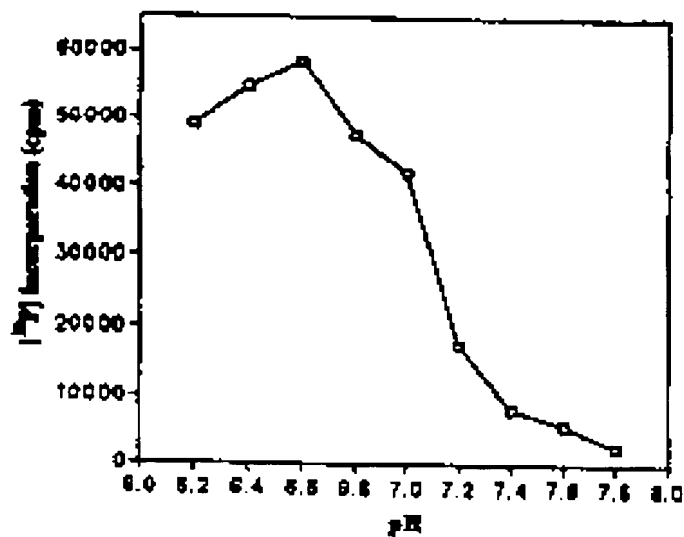


FIGURE 10

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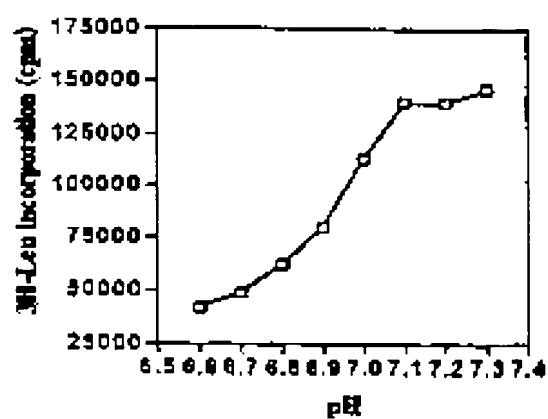


FIGURE 11

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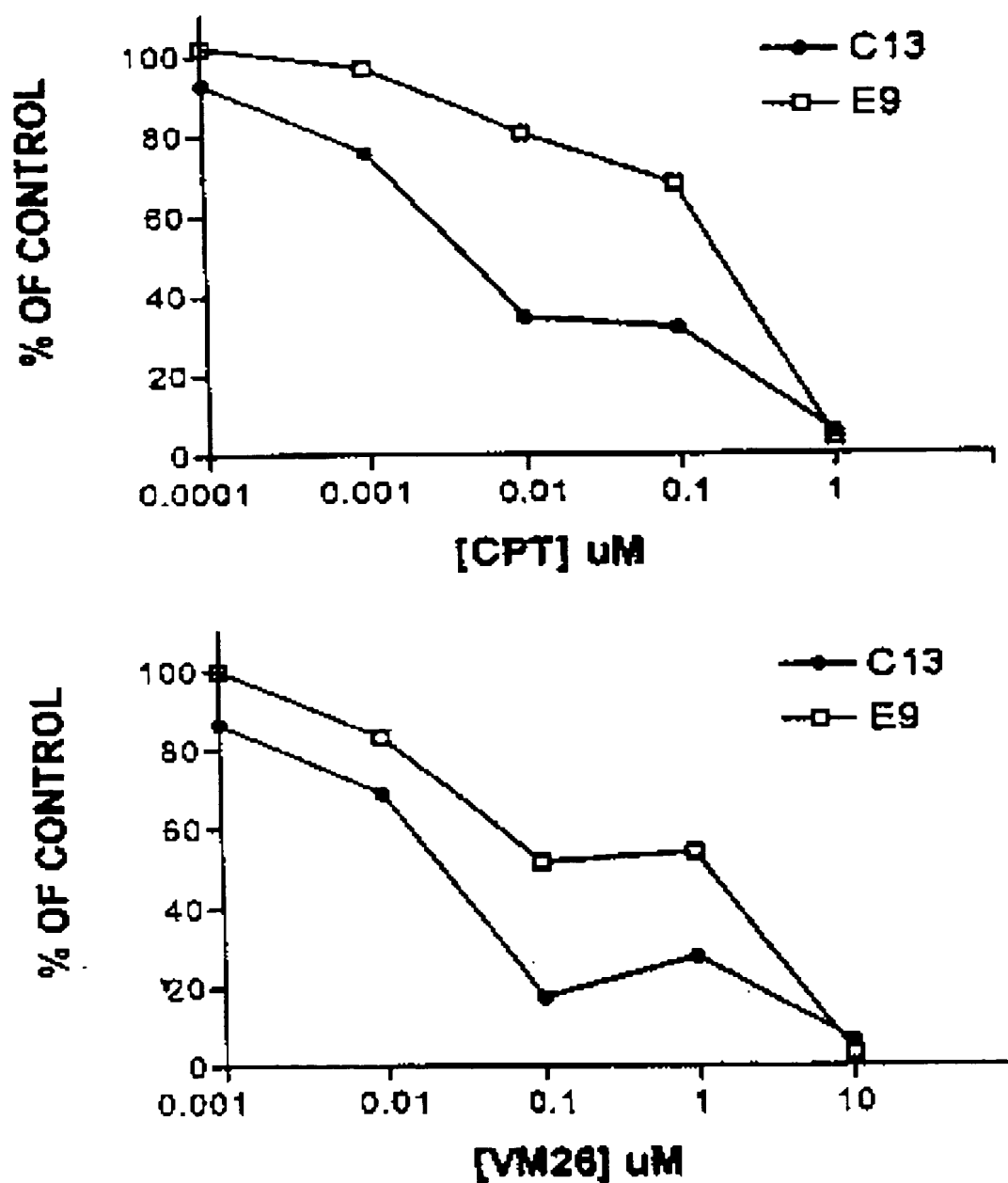


FIGURE 12

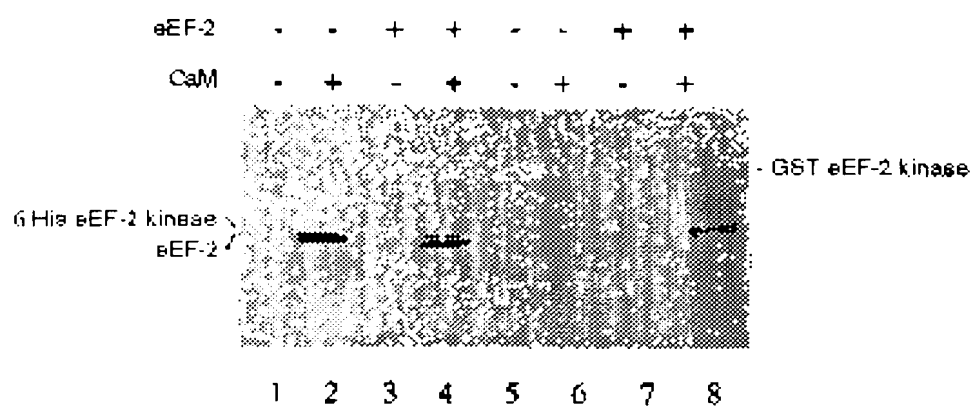


FIGURE 13

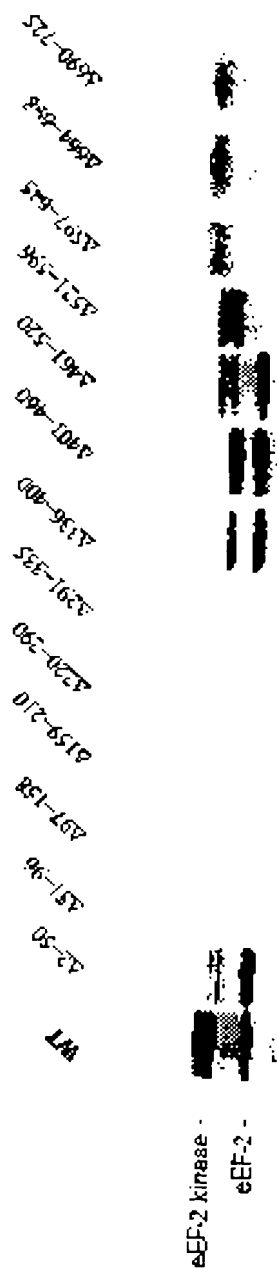


FIGURE 14

SUBSTITUTE SHEET (RULE 26)

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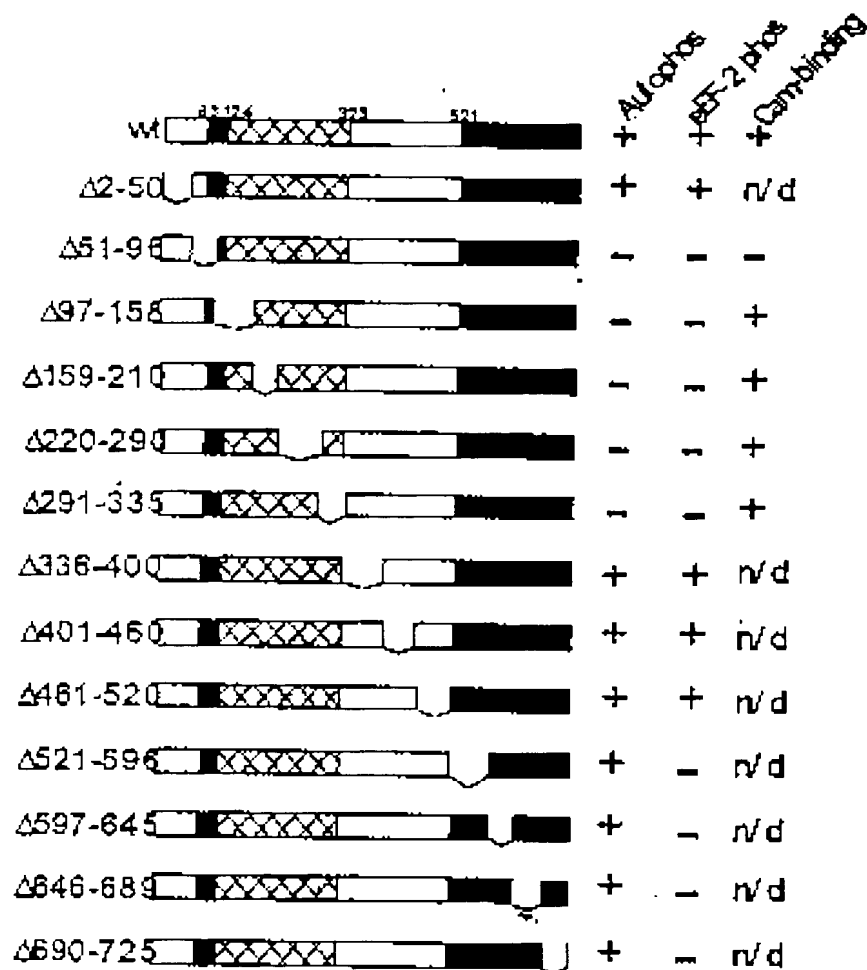


FIGURE 15

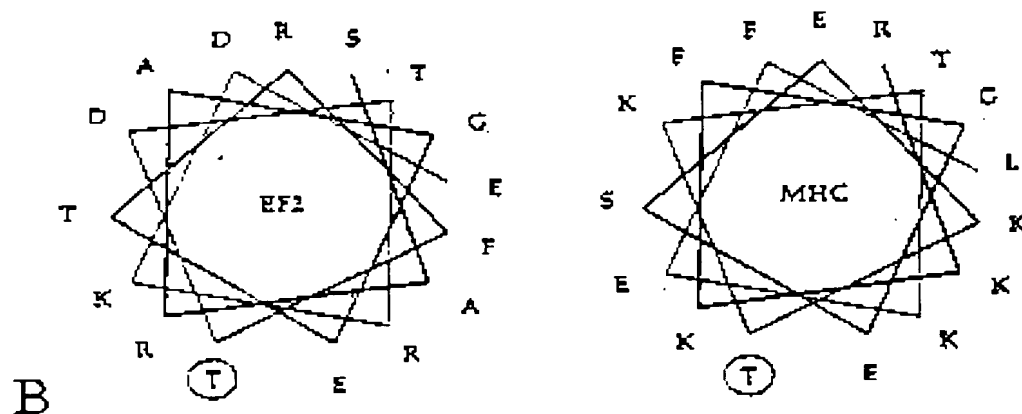
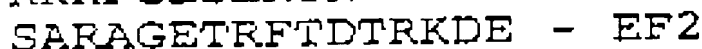
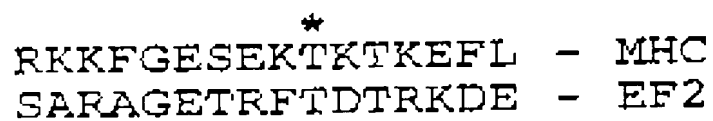
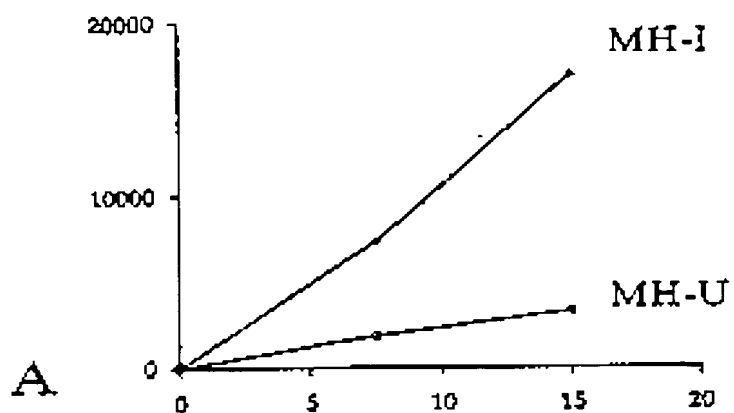


FIGURE 16

-1-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ryazanov, Alexey G.
Halt, William N.
Pavur, Karen S.

(ii) TITLE OF INVENTION: ELONGATION FACTOR 2 KINASE (EF-2 KINASE)
AND METHODS OF USE THEREFOR

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 26,742
(C) REFERENCE/DOCKET NUMBER: 601-1-078

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGSCAGACC AAGACCTCAT CTCCGCGCTG GAGGTGTG ATGGGGGCCA GTGCCXCCGA	60
GCCTGGCATT ATGCTGATTC TGATGGGGAC AGCGACGATG AGGAGGTTA CTTCATCTGC	120
CCCATCAGCG ATGACCCAG CTGGAACGAG AATGTCATT CCAGGTTAA TAACTACTAC	180
AGCAACCTAA CAAAAGTGA CCGCTATAGC TCCAGCGGT CCGCGGCAA CTCCTTCCAC	240
TTCAAGGAG CTTGGAAGCA CCGCATCCAG AACCCAGAG ACATGCCCGA CCCTTGGCT	300
GAGTTCCACC TGGAGATAT TCCCAUCCA CTTCTACTC GATACAGTA CACGCGCTC	360
ACCGGGGAAT GCTGGATCA TCAAGTCTC ATCAAGATG CATCTAGCC CTTCGGCCGA	420
GGAGCAATGA GGGATGCTT CCGGACGAG AAGCTCTCA ACTTCCTGCA TGCCGAGCAG	480
TGAGGGGCG CTCCAACTA CTTGHCAGG CTTACATCA AGCCCGTAGA CCGGATGTC	540
TACTTTGAGG AGCTCCCTCT ACAGATGGG GCCAAGCTCT GGGGGAGGA GTATAATCGG	600
CACAGCCCU CCAACAGGT GGACATCTG CAGATGTCA TCTCGAGCT GAGGACAGA	660
CCCGGCAAGC CACTCTTCCA CTTGGAGCA TACATCGAG GCAGTACAT CAAGTACAAC	720
TCCAACTCTG CTTTGTCCG TGATGACAA ATCCGACTGA TCGCGAGGC CTTCAGCCAC	780
TTCACTTTTG AGCGTTCCG CCAATCAGCT ATACTGCTG ACATCCAGG AGTTGGGAT	840
CTCTACACTG ACCACAGAT CCAACCGAG ACGGCCACTG ACTTGGAGA CCGCAACTA	900
GGTGTCCCGG GATGCGGCT CTCTTTCTAC TCTCATGCT CCAACCGCAT TTCCGAGCC	960
ATGGGCTTG CTCCCTTCA CTTCTCGCC CCGGAGAGCG ATCCAGTGAA TCAGAACACC	1020
AAGCTGCTGC ATCAGCCAA GACCATCTTG ACAGCAACAG AGCAAAATC TCCGAGCCCG	1080
CGAGTAAAGA CCTCTCTTG GAGCCGCGCA CCGTCTCTC GTCCCTTTC AAGAACTCT	1140
GGAGACGAGA ACATGAGCA CTGACCTTC GACTCTCTC CTCTTCCC ATCTTCGAC	1200


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AGACGACACA GCCAGAGGCT AGACCACCTC CMTGGGCCAG TCTTCACTGA CCTCGATAAC      1260
ATGGCATCCG GAGACCATGA TCATCTAGAC AACCAACGGG AGTCTACGAA TACTGGGGAC      1320
AGCGGATACC CCAGTGAGAA GCGGGGTGAG CTGGATGACC CTAGGCCCCC AGAACATGGC      1380
CACTATATAA GTAATCGGAA GTACGCTCT GTCCAGAGCA GCGTGGCCAG CTCTGACGG      1440
GTATGTGTAG AGAGGTGGAA TCTCTTCAC TCCTCCCGCC TCACCTTGGC GAGGGCTTTC      1500
GCGGTGGCCU TGGAGGTGCA AAGGCTTAAAT GCTTGGACC TCGTAAAGAA AATCGCCAGG      1560
TCATTTTTCG GGAAGCTTCA TCTGCTCATG CTGCGCTTAC AGGAGGTGG GCGCTTCTTC      1620
GAGAGGCGCG AGGACTGGA CCAGGAGTCT GCTGTCTTCC AACTGAGCA CGCAGCCAAC      1680
CTGGGCGAGC TGGACCCCAT CTTGCGCTG CCACTCATCT ACTCGAGTT GCGTCATCAC      1740
ATCCTAGCCG ATGTTCTCTT CAGCAGACA CAGACAACA AACCAAGG ATTTGATTAC      1800
TTACTAAAGG CCGCTTAAGC TGCGGACAGG CACTTCATCA TCTTAGTGGC GCGAGCTTTT      1860
GACTCTGCGC AGAACCTCAG CCGGACAGG TGCCAGACT GGTAGAGCC CTTGCACTGG      1920
TACCAACTG CCGTGGAGAT GACCGACTGT GATGAGGGCG GTGACTACCA CCGAATCCAG      1980
GACGAGCCCC GGTACATGAT GCTGGCCAGG GAGGCAGAGA TGCTETTCAC ACCAGCCCTAC      2040
GGGCTGAGGA AGGACCCGCA GAGATCAGG GACTTGTATA CCGAGGCAGC ACAGCCAGCC      2100
ATGGAAGGCA TGAGGGGCGG ACTGGCCAAC CAGTACTACC AAGAGGCTGA AGAGGCTGCG      2160
GCCCAGATGG AGGAATAA

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Asp	Glu	Asp	Leu	Ile	Phe	Arg	Leu	Glu	Gly	Val	Asp	Gly	Gly	1	5	10	15
Gln	Ser	Pro	Arg	Ala	Gly	His	Asp	Gly	Asp	Ser	Asp	Gly	Asp	Ser	Asp	20	25	30	
Asp	Gln	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp	Asp	Pro	Ser	Ser	35	40	45	
Asn	Gln	Asn	Val	Asn	Ser	Lys	Val	Asn	Lys	Tyr	Tyr	Ser	Asn	Leu	Thr	50	55	60	
Lys	Ser	Gln	Arg	Tyr	Ser	Ser	Ser	Gly	Ser	Pro	Ala	Asn	Ser	Phe	His	65	70	75	80
Phe	Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Gln	Lys	Ala	Lys	His	Met	Pro	85	90	95	
Asp	Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala	Thr	Glu	Arg	Ala	100	105	110	
Thr	Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp	Leu	Asp	Asp	Glu	115	120	125	
Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg	Gly	Ala	Met	Arg	130	135	140	
Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu	His	Ala	Gln	Gln	145	150	155	160
Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr	Ile	Glu	Pro	Val	165	170	175	
Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	Arg	Leu	Gln	Met	Glu	Ala	Lys	180	185	190	
Leu	Trp	Gly	Gln	Glu	Tyr	Asn	Arg	His	Lys	Pro	Pro	Lys	Gln	Val	Asp	195	200	205	
Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	Lys	Asp	Arg	Pro	Gly	Lys	Pro	210	215	220	
Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr	Ile	Lys	Tyr	Asn	225	230	235	240
Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg	Leu	Thr	Pro	Gln	245	250	255	
Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	Gln	Leu	Ile	Val				

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260										265					270				
Val	Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp	Pro	Gln	Ile	His				
	275						280					285							
Thr	Glu	Thr	Gly	Thr	Asp	Phe	Gly	Asp	Gly	Asn	Leu	Gly	Val	Arg	Gly				
	290					295					300								
Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	Cys	Asn	Arg	Ile	Cys	Glu	Ser				
305					310					315					320				
Met	Gly	Leu	Ala	Pro	Phe	Asp	Leu	Ser	Pro	Arg	Glu	Arg	Asp	Ala	Val				
				325					330					335					
Asn	Gln	Asn	Thr	Lys	Leu	Leu	Gln	Ser	Ala	Lys	Thr	Ile	Leu	Arg	Gly				
			340					345					350						
Thr	Glu	Glu	Lys	Cys	Gly	Ser	Pro	Arg	Val	Arg	Thr	Leu	Ser	Gly	Ser				
	355						360					365							
Arg	Pro	Pro	Leu	Leu	Arg	Pro	Leu	Ser	Glu	Asn	Ser	Gly	Asp	Glu	Asn				
	370					375					380								
Met	Ser	Asp	Val	Thr	Phe	Asp	Ser	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Ala				
385					390					395					400				
Thr	Pro	His	Ser	Gln	Lys	Leu	Asp	His	Leu	His	Trp	Pro	Val	Phe	Ser				
			405					410						415					
Asp	Leu	Asp	Asn	Met	Ala	Ser	Arg	Asp	His	Asp	His	Leu	Asp	Asn	His				
			420					425					430						
Arg	Glu	Ser	Glu	Asn	Ser	Gly	Asp	Ser	Gly	Tyr	Pro	Ser	Glu	Lys	Arg				
	435						440					445							
Gly	Glu	Leu	Asp	Asp	Pro	Glu	Pro	Arg	Glu	His	Gly	His	Ser	Tyr	Ser				
	450					455						460							
Asn	Arg	Lys	Tyr	Glu	Ser	Asp	Glu	Asp	Ser	Leu	Gly	Ser	Ser	Gly	Arg				
465					470					475					480				
Val	Cys	Val	Glu	Lys	Trp	Asu	Leu	Leu	Asn	Ser	Ser	Arg	Leu	His	Leu				
				485					490					495					
Pro	Arg	Ala	Ser	Ala	Val	Ala	Leu	Glu	Val	Gln	Arg	Leu	Asn	Ala	Leu				
			500					505					510						
Asp	Leu	Glu	Lys	Lys	Ile	Gly	Lys	Ser	Ile	Leu	Gly	Lys	Val	His	Leu				
	515						520					525							
Ala	Met	Val	Arg	Tyr	His	Glu	Gly	Gly	Arg	Phe	Cys	Glu	Lys	Gly	Glu				

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530	535	540
Glu Trp Asp Glu Glu Ser Ala Val Phe His Leu Glu His Ala Ala Asn		
545	550	555 560
Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Glu		
	565	570 575
Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu		
	580	585 590
Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly		
	595	600 605
Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe Asp Ser Gly Glu		
	610	615 620
Asp Leu Ser Pro Asp Arg Cys Glu Asp Trp Leu Glu Ala Leu His Trp		
	625	630 635 640
Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu Gly Gly Glu Tyr		
	645	650 655
Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu Ala Arg Glu Ala		
	660	665 670
Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys Asp Pro Gln Arg		
	675	680 685
Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala Met Glu Ala Met		
	690	695 700
Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala Glu Glu Ala Trp		
	705	710 715 720
Ala Gln Met Glu Glu		
		725

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Mus musculus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGTCAGACG AAGACCTCAT CTCTTCCTTC GAAGCTGTTG ACGGTGGCAG GTGCTCCCGA	60
GCTGGCCACA ATGCGGACTC TCACACAGAC AATGAAGATG ATGAGGGCTA TTTATATTC	120
CCCATCACTG ATGACACAT CTCCAAATCA AATGTGAGCT CCATAGTCCA GAGCTACTAT	180
AGCAACCTAA CAAAAACAA ATGCGGCTTC ACAGGCTCAC CAGCCAGCTC CTTCCTCTTC	240
AAGGAAGCCT GGAACCTTC GATGAGAAA CCAACACACA TGCCGACCC CTGGGCTGAA	300
TTCATCTTC AUGACATGC CACAGAACAT GCTACTCCCG ACAGGTACAA CGCTGTCCAC	360
GGGGAATGCG TGAAGAGCA GGTCTGATC AAGATGCGT CTGAGGCTT GGGCCTGGA	420
CGAATGAGCG ATGCTCTCAG GACGAGAAA CTCTCCAACT TCTTCGACCG CCAGCAATGG	480
AAGCGGCTCT CCACTACGT GGCCTAGGCG TACCTGAGC CGGTGACAG GAGCTGTAC	540
TTTGAGGATG TGCAGCTCCA GATGGAGGCG AAGCTCTGGG GGGAGGATTA CATCGGCACT	600
AGCCCCCCTA AGCAGGTGGA TATCATCGAC ATGTGATGTA TTGAGTAAA GGACAGACCA	660
GGCCAGCCCC TCTTCACCTT CGACCACTAC ATTCAGGGCA AGTACATCAA GTACAATTCC	720
AACTCAGGCT TTGTCCGTA TCACAAATC CCACTAACCT CACAGGCTT CAGCCATTC	780
ACATTGAGC GTCTGCTCA TCACTCATT CTAGTGACA TCCAGGGTGT GGTGACCTT	840
TATACCGACC CACAGATCCA CACTGAGAAA AGCACTGACT TTCCGATCC TAACTTTGGT	900
GTCCGGGAAA TCCCTCTCTT CTCTACTCT CATGCTGCA ACCGATTTG TCACAGCAAG	960
GGCTTACGC CTTTGAAGT CTCCCCACGG GACAGGATG CGGTAAATCA GAGCACCAGC	1020
CTATTGCAAT CAGCCAGAC CATCTTGAGG GGCACAGAG AGAAGTGTGG GAGTCTCCCG	1080
ATAAGGACAC TCTCTAGCAG CCGGCCCCCT TTGCTCTTC GCTGCTCAGA GAATCTCGCG	1140
GATCAGACAA TGAATGACGT GACCTTTGAC TCTCTGCTCT CTTCCCCGTC TTCAGCTACA	1200
CCACACAGCC AGAACTGGA CCACCTCCAT TGGCCAGTGT TTGGTGACCT CGATACATG	1260
GGCCCTAGAG ACCATGACCG TATGACCAAT CACCGGACT CTGAGATAG TGGGGACAGT	1320
GGGTATCCAA GCGAGAAAGC AAGTACCTG CATCATCTTC ACUCCTGAGA ACAAGGCCAC	1380

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TCCATCGGCA ACCGAGGCA TCAATCTCAC GAGGATAGCC TGGGCGCTC TGGACGCGTC 1440
TGTGTGGAGA CGTGGAACTT GGTCAATCCC TCCGCGCTGC ACCTGCGGAG GCGCTCGGCC 1500
GTGGCCCTAG AAGTGCACAG CTTAATGCC CTGGAUCTTG GAGGAAATAT CGGGAAGTCT 1560
GTTTTCGGCA AATTTCATTT GGCATGCTG CATACACAG AGGCGGGGCG CTTCTGCGAG 1620
AAGGATGAGG AGTGGGATCG AGACTCAGCC ATCTTCATC TGAACGATCC AGCTGACCTG 1680
GGAGAACTGG AGGCCATGCT GGGCTAGGC CTCATGTACT CTCAGCTGCC CCACTACATC 1740
CTGGCTGATG TCTCTCTGAA GGAGACAGAG GAGAACAGA CAAAGGCTT TGATTACTTA 1800
CTCAAGGCGG CAGAAGCTGG TGACAGGCTT TCCATGATTT TACTGCGCCG ACCTTTTGAC 1860
ACTGCGCTGA ACCTCAGCCC AGACAGGTGT CAGGACTGCT CGAAGGCTT GCACTGCTAC 1920
AACACAGCCC TGGAGACACC AGACTCGGAT GAGGGCGGGG AGTACGATG GATACAGGAC 1980
GAGCCCCAGT AGGCACTGCT GCGCGCGGAG CCGGAGATGC TGTCAACCG GGGATTTGGA 2040
CTGGACAAGA ACCCCCAAG ATCAGGAGAT TTCTACGCC AGCCAGCTGA GCGAGCATG 2100
GAAGCCATGA ACCCGCGGCT AGCCACAGG TACTACAGA ACCCGCAAGA GGCCTGGGCC 2160
CAGATGGAGG AATAA 2175

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: M08 mmedlin

(x) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ala Asp Glu Asp Leu Ile Phe Cys Leu Glu Gly Val Asp Gly Gly
1           5           10           15

Arg Cys Ser Arg Ala Gly His Asn Ala Asp Ser Asp Thr Asn Ser Asp

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20					25					30					
Asp	Asp	Glu	Gly	Tyr	Phe	Ile	Cys	Pro	Ile	Thr	Asp	Asp	His	Met	Ser
	35						40					45			
Asn	Gln	Asn	Val	Ser	Ser	Lys	Val	Gln	Ser	Tyr	Tyr	Ser	Asn	Leu	Thr
	50					55					60				
Lys	Thr	Glu	Cys	Gly	Ser	Thr	Gly	Ser	Pro	Ala	Ser	Ser	Phe	His	Phe
	65					70					75				80
Lys	Glu	Ala	Trp	Lys	His	Ala	Ile	Glu	Lys	Ala	Lys	His	Met	Pro	Asp
				85					90					95	
Pro	Trp	Ala	Glu	Phe	His	Leu	Glu	Asp	Ile	Ala	Thr	Glu	His	Ala	Thr
			100					105					110		
Arg	His	Arg	Tyr	Asn	Ala	Val	Thr	Gly	Glu	Trp	Leu	Lys	Asp	Glu	Val
			115					120					125		
Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	Phe	Gly	Arg	Gly	Ala	Met	Arg	Glu
	130						135				140				
Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	Asn	Phe	Leu	His	Ala	Gln	Gln	Trp
	145					150					155				160
Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	Lys	Arg	Tyr	Ile	Glu	Pro	Val	Asp
				165					170					175	
Arg	Ser	Val	Tyr	Phe	Glu	Asp	Val	Gln	Leu	Gln	Met	Glu	Ala	Lys	Leu
			180					185					190		
Trp	Gly	Glu	Asp	Tyr	Asn	Arg	His	Lys	Pro	Pro	Lys	Gln	Val	Asp	Ile
			195				200					205			
Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	Lys	Asp	Arg	Pro	Gly	Gln	Pro	Leu
	210					215					220				
Phe	His	Leu	Glu	His	Tyr	Ile	Glu	Gly	Lys	Tyr	Ile	Lys	Tyr	Asn	Ser
	225					230					235				240
Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	Asn	Ile	Arg	Leu	Thr	Pro	Gln	Ala
				245					250					255	
Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	Gln	Leu	Ile	Val	Val
			260					265					270		
Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp	Pro	Gln	Ile	His	Thr
	275						280					285			
Glu	Lys	Gly	Thr	Asp	Phe	Gly	Asp	Gly	Asn	Leu	Gly	Val	Arg	Gly	Met

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290	295	300
Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Gln Ser Met 305	310	315 320
Gly Leu Thr Pro Phe Asp Leu Ser Pro Arg Glu Gln Asp Ala Val Asn 325	330	335
Gln Ser Thr Arg Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly Thr 340	345	350
Glu Glu Lys Cys Gly Ser Pro Arg Ile Arg Thr Leu Ser Ser Ser Arg 355	360	365
Pro Pro Leu Leu Leu Arg Leu Ser Glu Asn Ser Gly Asp Glu Asn Met 370	375	380
Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser Pro Ser Ser Ala Thr 385	390	395 400
Pro His Ser Glu Lys Leu Asp His Leu His Trp Pro Val Phe Gly Asp 405	410	415
Leu Asp Asn Met Gly Pro Arg Asp His Asp Arg Met Asp Asn His Arg 420	425	430
Asp Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro Ser Glu Lys Arg Ser 435	440	445
Asp Leu Asp Asp Pro Glu Pro Arg Glu His Gly His Ser Asn Gly Asn 450	455	460
Arg Arg His Glu Ser Asp Glu Asp Ser Leu Gly Ser Ser Gly Arg Val 465	470	475 480
Cys Val Glu Thr Trp Asn Leu Leu Asn Pro Ser Arg Leu His Leu Pro 485	490	495
Arg Pro Ser Ala Val Ala Leu Glu Val Glu Arg Leu Asn Ala Leu Asp 500	505	510
Leu Gly Arg Lys Ile Gly Lys Ser Val Leu Gly Lys Val His Leu Ala 515	520	525
Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys Glu Lys Asp Glu Glu 530	535	540
Trp Asp Arg Glu Ser Ala Ile Phe His Leu Glu His Ala Ala Asp Leu 545	550	555 560
Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Gln Leu		

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	565		570		575										
Pro	His	His	Ile	Leu	Ala	Asp	Val	Ser	Leu	Lys	Glu	Thr	Glu	Glu	Asn
	580							585					590		
Lys	Thr	Lys	Gly	Phe	Asp	Tyr	Leu	Leu	Lys	Ala	Ala	Glu	Ala	Gly	Asp
	595						600					605			
Arg	His	Ser	Met	Ile	Leu	Val	Ala	Arg	Ala	Phe	Asp	Thr	Gly	Leu	Asn
	610					615					620				
Leu	Ser	Pro	Asp	Arg	Cys	Gln	Asp	Trp	Ser	Glu	Ala	Leu	His	Trp	Tyr
	625				630					635				640	
Asn	Thr	Ala	Leu	Glu	Thr	Thr	Asp	Cys	Asp	Glu	Gly	Gly	Glu	Tyr	Asp
			645					650					655		
Gly	Ile	Gln	Asp	Glu	Pro	Gln	Tyr	Ala	Leu	Leu	Ala	Arg	Glu	Ala	Glu
		660					665						670		
Met	Leu	Leu	Thr	Gly	Gly	Phe	Gly	Leu	Asp	Lys	Asn	Pro	Gln	Arg	Ser
	675					680						685			
Gly	Asp	Leu	Tyr	Thr	Gln	Ala	Ala	Glu	Ala	Ala	Met	Glu	Ala	Met	Lys
	690				695						700				
Gly	Arg	Leu	Ala	Asn	Gln	Tyr	Tyr	Glu	Lys	Ala	Glu	Glu	Ala	Trp	Ala
	705			710					715					720	
Gln	Met	Glu	Glu												

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULAR TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Dictyostelium discoideum
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGTTTAAATA TAAAGAAAGAG	AAAGAGAGAGT ATAACAGGTA	TACCAACCAAT AAATGTTAAT	60
AGTCCACAAAT CAGTTCACAT	GAGTGGAGCA ITGCAATCAC	CATTGATTAC ACCCAATTCA	120
CCAAATTTTG TTTCACCTCA	ATGTCCATTC AAAAGTTTG	GATCTACTAC TTCTTTAGTT	180
TCAAAGGCAG AGTTTGATAA	TCACCTAAG GATGAGCAC	AATTTCAATT ACAATTGGCA	240
GTGGAGAAAT TTGATCACTA	ATTGAAITTA CACACACAA	TGATGGCACA TTTTACTCAC	300
CAATGGAGG ATCAATTACA	CAAAACAATG AAGGTCTAC	GTATTCATAC AGATAGTTTA	360
CCCCCTAATC TTCAAGCCAA	ATTGGATGAA CCAATTCAAA	AATGTATGGC TTTTCTAAA	420
ABGCTTCAAC AACAAACACA	ACAATTGGCC AAAACATTAA	TCACCTAACA AATTCAGAG	480
ABCABAACA CCTCTTCAAC	TTTAGTTAAA GCTCTATTA	GTGGTGGTGG TGGTAGTGGT	540
CCCCATCATT GTTTTGAATG	CCCAAGATA TCATCAATCT	CAACTAGTAA ACAGAAITTA	600
CAACAAGAAAT TACAATCATT	ATCAATTAAA ATGAAGAAAG	AATTCAACAA ATTATCCGAT	660
GACCTATCAC AAAAATTAGA	ACGTTCAACA GGTATATAG	ATATTAAAAT AAAGAGAAATC	720
GAAGGTGAAG TTAATGAAA	GATTGATAAA CGTCAATTGG	TCTCTACGAT CCAATGATTCA	780
ATTGGAAAGA AACACAGATC	CATGSETTAT ACATTGGAGA	GTTCATTCAT TAAAAAGGTT	840
GAGGAGAAAG AGAAGAGAA	ATCAGAAACA AATCACTTC	TCTTTGATTC AAGATTGAA	900
TCCTTAAAAG ATAAGAITTA	AATCAATTGA ACTCAACAAT	TGGATACCTC ATCAGAGGTT	960
AGAAATTTGA AATTAGAAAG	TACAAGTACT CCAATTTTAA	TGGCAGGTCT TAATGGTACC	1020
TCTGCTACAC CTTCACTATC	TTCTCACTTT ATTCATCTCT	CTCTTTCTTC CCGTGCATAC	1080
AATATCAACA AAGATGAAT	CATGGAGAG GTTAAAAAG	TAGAAGACAA ACTTCAAAAG	1140
AAAATTCCCTC AAGAGATTGA	TAATACAAA GCTGAACCTCT	CAAGCTTCA ACGTTCCGTT	1200
AAAGATAATC CTAGTGAAAT	TGAAGGTTTG GAAGAAGATT	CTAACAATCA ATTGATATAA	1260
CAAGACAATA AGATCAACA	AGTTGAGGAT GATTTGAAA	AGAGTATTC ATTACTTTTC	1320
TTAATGCAAA ATAACTTCAA	GAAATATAAT GAATTTGTTG	ATAGAGAACG TGATCGTGA	1380
AGTGAACGTT TGAAACTTCA	AGATTCTATC AAACGTTTAG	AACAAATCA AAGGAAATC	1440
GAAGCTGAAA TTCAAGAGG	TAATGAACAA GTTGAAGTG	TTTACGTGA GGAAGCTTCA	1500
ATCTACCAA TTAGTTCACT	TCCAAATCA CCAATCAAA	CAAAAGTTT ATCGATTATT	1560

TTAAATTTCAC CACCAATGAC TTCACACACAC TCATCACCAA AGATTCAAGA TCTTCTCTCA	1620
AGTAGTGGTA GTAGTAGTGT TAGTGGTATA AATATTTCTT CTGAAACCCG TCAATGGGT	1680
ATTCTTTGGG AATTTGATCC AATCATTTAC AATGGATTA GATTATCAAT GAAGCTAAAG	1740
GTAGAAAGAA AACCATTTCC AACAGGTGCT CTTAGAGAGG CTTATCATAC CGTTTCAATT	1800
GGTGTGGAA CCGATCABA TTATCCATTA GGTACAAACA CCAATTATT CCCACCAATT	1860
GAAATGATTT CACCAATTTG AAAGATAAT GAGCCAAACA CTAATTGAA GAATGGTACA	1920
AAATTTGTCT TCAAACTCTA CAAAGAGAA GGTGAACAA AAGCTAGCAG AGAATTATAC	1980
TCTCAGCATC TTAAGATGCA ATGGTCTGT AGAGATTGGG GTAAATAAAT CATTCAAAAG	2040
AAACCAACAA AGAAATTTGA ATTCCTTATG TCTGGGGTGG TAGAGTTAAT CCATACATCT	2100
CGTTCTTCCA ATGGTCAACC AATAGTTTGT TCCATTGAA CATTATTGGT TGTGAATTC	2160
AAAAAGATA ATTCAAATTA TGGTGCAGTT TTAACCAATC GTTCAACTCC ACAAGCATTC	2220
TCTCATTTCA CCTATGAAC TCAAAATAAA CAAATGATCG TTGTGGATAT TCAAGGTGTT	2280
GATGATCTTT ACCTGATCC TCAAAATCAT ACACCCGATG GTAAAGGATT TGTCTTGGT	2340
AATCTTGGTA AAGCAGGTAT CAATAAATTC ATCAUUAUAC ACAATGTAA TGCTGTTGT	2400
GCTCTTTTNG ATTTAGATCT TAAATTTGCT CTTCTACTAT CTGCAATAA TAGAAACAA	2460
CTTCACCAAG GTACTATGCT TATGCTAGAT ATTTCTCCAC AACCTATGCC ATCTGATAAC	2520
ACCATTAAG TGGGTGCAAA ACAACTTCCA AAAGCTGAAT TCTCAGAGAA AGATCTCAA	2580
TGTGTTAGUA CCATTCGAA TTTCCGTGAA CGGTTAATCT CCATCCCAT TTTTGATAAT	2640
CAAAAGTTAT TATCCGCTGG TTATGGTGAT GTACCTATA GAGTTTTCGA TGTCAATCAC	2700
AATTCGAAT CTTTATACAC TGTCAATGGT CATAGAAAT CAATTGAAG TATGCTTCT	2760
AATAGTAATT ACATTTTCAC TTUATCACT GATAACCCA TCAAGTTCA TATCATTCGT	2820
ATGATTAACA CCAATGTAT AGAGACATTC GTTGGTACA CTGGTGAGT TAATTGTGTC	2880
GTGACCAATG AAAAATATCT TTTCAGTTGT AGTTATGATA AAATATCAA GGTTTGGGAT	2940
TTGTCAACCT TTAAAGAAAT TAAATCATTT GAGGTGTTT ATACAAAGTA CATTAAACA	3000
TTGGCTTTGA GTGGACGTTA TCTTTTATCT GGTCTAAGC ATCAAAATCAT TTACGTTTGG	3060
GATACTGAA CACTTAGTAT CTTTTTCAAT ATGCAAGCTC ATCAAGATTC GGTACTCTCT	3120

GTTCATTGTA CCGCTAGTTA TCTTTTCTCA ACCTCAAAAG ATATATGTCAT CAAGATTTCG 3180
 GATCTCTCAAT ATTTCAGTTG TATCGATACT CTAAAAGGTC ATTGGGAATTC TGTCTCAAGT 3240
 TGTGTCTGTA AAGATCGTTA TTTATACAGT GGTTCGGAAG ATATATTCAT CAAGATTTCG 3300
 GATCTCGATA CACTTGAATG TGTTCACACC ATTCCAAAAT CTCATTCTTT GGGTGTAAAA 3360
 TGTTTAATGG TTTCAATTA TCAAAATCATT TCTGCTCCTT TCGATGCTTC AATTAAAGTT 3420
 TGGGAATGCC AATCGAATA ATCTTTGTAA ATTTTGTGTA AAAAA 3465

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Dictyostelium discoideum

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Phe	Asn	Ile	Lys	Lys	Arg	Lys	Glu	Ser	Ile	Thr	Gly	Ile	Pro	Pro	1	5	10	15
Ile	Asn	Val	Asn	Ser	Pro	Gln	Ser	Val	Pro	Leu	Ser	Gly	Thr	Leu	Gln	20	25	30	
Ser	Pro	Leu	Ile	Thr	Pro	Asn	Ser	Pro	Asn	Phe	Val	Ser	Arg	Gln	Cys	35	40	45	
Pro	Phe	Lys	Lys	Phe	Gly	Cys	Ser	Ser	Phe	Leu	Val	Ser	Lys	Ala	Glu	50	55	60	
Phe	Asp	Asn	His	Leu	Lys	Asp	Asp	Ala	Gln	Phe	His	Leu	Gln	Leu	Ala	65	70	75	80
Val	Glu	Lys	Phe	Asp	His	Gln	Phe	Asp	Leu	His	Thr	Gln	Leu	Met	Ala	85	90	95	
His	Phe	Thr	Gln	Gln	Met	Glu	Asp	Gln	Leu	Glu	Lys	Thr	Met	Lys	Val	100	105	110	

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Val	Arg	Asn	His	Thr	Asp	Ser	Leu	Gly	Gly	Asn	Val	Gln	Thr	Lys	Leu
		115					120					125			
Asp	Glu	Gly	Ile	Glu	Lys	Cys	Met	Ala	Phe	Ala	Lys	Lys	Val	Glu	Gln
	130					135					140				
Gln	Gln	Gln	Gln	Leu	Ala	Lys	Arg	Leu	Ile	Thr	Gln	Gln	Ile	Gln	Glu
145					150					155					160
Lys	Lys	Ser	Thr	Ser	Ser	Pro	Leu	Val	Lys	Gly	Gly	Ile	Ser	Gly	Gly
				165					170					175	
Gly	Gly	Ser	Gly	Gly	Asp	Asp	Ser	Phe	Asp	Gly	Ala	Asn	Ile	Ser	Ser
			180					185					190		
Met	Ser	Thr	Ser	Lys	Gln	Glu	Leu	Gln	Gln	Glu	Leu	Gln	Ser	Leu	Ser
		195					200					205			
Ile	Lys	Met	Lys	Lys	Glu	Leu	Thr	Glu	Leu	Ser	Asp	Glu	Leu	Ser	Gln
	210					215					220				
Lys	Leu	Glu	Arg	Ser	Thr	Gly	Asn	Ile	Asp	Thr	Lys	Ile	Lys	Arg	Ile
225					230					235					240
Glu	Gly	Glu	Val	Asn	Glu	Lys	Ile	Asp	Lys	Arg	Gln	Leu	Val	Ser	Thr
			245						250					255	
Ile	Asp	Asp	Ser	Ile	Gly	Lys	Lys	Thr	Asp	Ser	Ile	Gly	Tyr	Thr	Leu
			260					265					270		
Gln	Ser	Ser	Ile	Ile	Lys	Lys	Val	Glu	Gln	Lys	Glu	Lys	Lys	Lys	Ser
		275					280					285			
Glu	Gln	Asn	Gln	Leu	Leu	Phe	Asp	Ser	Lys	Ile	Glu	Ser	Leu	Lys	Asp
	290					295					300				
Lys	Ile	Lys	Ile	Ile	Glu	Thr	Gln	Gln	Leu	Asp	Thr	Ser	Ser	Gln	Val
305					310					315					320
Arg	Lys	Leu	Lys	Leu	Glu	Ser	Thr	Ser	Ser	Gly	Asn	Leu	Met	Ala	Gly
			325						330					335	
Leu	Asn	Gly	Thr	Ser	Gly	Arg	Pro	Ser	Ser	Ser	Ser	His	Phe	Ile	Pro
			340					345					350		
Ser	Ser	Val	Ser	Ala	Ala	Ala	Asn	Asn	Ile	Asn	Lys	Asn	Gln	Ile	Met
		355					360					365			
Glu	Glu	Val	Lys	Lys	Val	Glu	Gln	Lys	Leu	Gln	Lys	Lys	Ile	Arg	Glu
	370					375					380				

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Glu Ile Asp Asn Thr Lys Ala Glu Leu Ser Lys Val Glu Arg Ser Val
 305 390 395 400
 Lys Asp Asn Arg Ser Glu Ile Glu Gly Leu Glu Lys Asp Cys Lys Asn
 405 410 415
 Glu Phe Asp Lys Gln Asp Asn Lys Ile Lys Gln Val Glu Asp Asp Leu
 420 425 430
 Lys Lys Ser Asp Ser Leu Leu Leu Leu Met Gln Asn Asn Leu Lys Lys
 435 440 445
 Tyr Asn Glu Phe Val Asp Arg Glu Arg Asp Arg Glu Ser Glu Arg Leu
 450 455 460
 Lys Leu Gln Asp Ser Ile Lys Arg Leu Glu Gln Asn Gln Lys Lys Ile
 465 470 475 480
 Glu Ala Glu Ile Gln Glu Gly Asn Glu Gln Val Glu Arg Val Leu Arg
 485 490 495
 Glu Glu Ala Ser Ile Ser Pro Ile Ser Ser Val Pro Lys Ser Pro Ile
 500 505 510
 Thr Thr Lys Arg Ser Ser Ile Ile Leu Asn Ser Pro Pro Met Thr Ser
 515 520 525
 Gln Gln Ser Ser Pro Lys Ile Gln Asp Leu Leu Ser Ser Ser Gly Ser
 530 535 540
 Ser Ser Val Ser Gly Ile Asn Ile Ser Ser Glu Thr Gly Glu Met Gly
 545 550 555 560
 Ile Leu Trp Glu Phe Asp Pro Ile Ile Asn Lys Trp Ile Arg Leu Ser
 565 570 575
 Met Lys Leu Lys Val Glu Arg Lys Pro Phe Ala Glu Gly Ala Leu Arg
 580 585 590
 Glu Ala Tyr His Thr Val Ser Leu Gly Val Gly Thr Asp Glu Asn Tyr
 595 600 605
 Pro Leu Gly Thr Thr Thr Lys Leu Phe Pro Pro Ile Glu Met Ile Ser
 610 615 620
 Pro Ile Ser Lys Asn Asn Glu Ala Met Thr Gln Leu Lys Asn Gly Thr
 625 630 635 640
 Lys Phe Val Leu Lys Leu Tyr Lys Lys Glu Ala Glu Gln Gln Ala Ser
 645 650 655

Arg	Glu	Leu	Tyr	Phe	Glu	Asp	Val	Lys	Met	Gln	Met	Val	Cys	Arg	Asp
660				665				670							
Trp	Gly	Asn	Lys	Phe	Asn	Gln	Lys	Lys	Pro	Pro	Lys	Lys	Ile	Glu	Phe
675				680				685							
Leu	Met	Ser	Trp	Val	Val	Glu	Leu	Ile	Asp	Arg	Ser	Pro	Ser	Ser	Asn
690				695				700							
Gly	Gln	Pro	Ile	Leu	Cys	Ser	Ile	Glu	Pro	Leu	Leu	Val	Gly	Glu	Phe
705				710				715				720			
Lys	Lys	Asn	Asn	Ser	Asn	Tyr	Gly	Ala	Val	Leu	Thr	Asn	Arg	Ser	Thr
725				730				735							
Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Tyr	Glu	Leu	Ser	Asn	Lys	Gln	Met
740				745				750							
Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Asp	Asp	Leu	Tyr	Thr	Asp	Pro	Gln
755				760				765							
Ile	His	Thr	Pro	Asp	Gly	Lys	Gly	Phe	Gly	Leu	Gly	Asn	Leu	Gly	Lys
770				775				780							
Ala	Gly	Ile	Asn	Lys	Phe	Ile	Thr	Thr	His	Lys	Cys	Asn	Ala	Val	Cys
785				790				795				800			
Ala	Leu	Leu	Asp	Leu	Asp	Val	Lys	Leu	Gly	Gly	Val	Leu	Ser	Gly	Asn
805				810				815							
Asn	Lys	Lys	Gln	Leu	Gln	Gln	Gly	Thr	Met	Val	Met	Pro	Asp	Ile	Leu
820				825				830							
Pro	Glu	Leu	Met	Pro	Ser	Asp	Asn	Thr	Ile	Lys	Val	Gly	Ala	Lys	Gln
835				840				845							
Leu	Pro	Lys	Ala	Glu	Phe	Ser	Lys	Lys	Asp	Leu	Lys	Cys	Val	Ser	Thr
850				855				860							
Ile	Gln	Ser	Phe	Arg	Glu	Arg	Val	Asn	Ser	Ile	Ala	Phe	Phe	Asp	Asn
865				870				875				880			
Gln	Lys	Leu	Leu	Cys	Ala	Gly	Tyr	Gly	Asp	Gly	Thr	Tyr	Arg	Val	Phe
885				890				895							
Asp	Val	Asn	Asp	Asn	Trp	Lys	Cys	Leu	Tyr	Thr	Val	Asn	Gly	His	Arg
900				905				910							
Lys	Ser	Ile	Glu	Ser	Ile	Ala	Cys	Asn	Ser	Asn	Tyr	Ile	Phe	Thr	Ser
915				920				925							

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Ser Pro Asp Asn Thr Ile Lys Val His Ile Ile Arg Ser Gly Asn Thr
 930 935 940
 Lys Cys Ile Glu Thr Leu Val Gly His Thr Gly Glu Val Asn Cys Val
 945 950 955 960
 Val Ala Asn Glu Lys Tyr Leu Phe Ser Cys Ser Tyr Asp Lys Thr Ile
 965 970 975
 Lys Val Trp Asp Leu Ser Thr Phe Lys Glu Ile Lys Ser Phe Glu Gly
 980 985 990
 Val His Thr Lys Tyr Ile Lys Thr Leu Ala Leu Ser Gly Arg Tyr Leu
 995 1000 1005
 Phe Ser Gly Gly Asn Asp Gln Ile Ile Tyr Val Trp Asp Thr Glu Thr
 1010 1015 1020
 Leu Ser Met Leu Phe Asn Met Glu Gly His Gln Asp Trp Val Leu Ser
 1025 1030 1035 1040
 Leu His Cys Thr Ala Ser Tyr Leu Phe Ser Thr Ser Lys Asp Asn Val
 1045 1050 1055
 Ile Lys Ile Trp Asp Leu Ser Asn Phe Ser Cys Ile Asp Thr Leu Lys
 1060 1065 1070
 Gly His Trp Asn Ser Val Ser Ser Cys Val Val Lys Asp Arg Tyr Leu
 1075 1080 1085
 Tyr Ser Gly Ser Glu Asp Asn Ser Ile Lys Val Trp Asp Leu Asp Thr
 1090 1095 1100
 Leu Glu Cys Val Tyr Thr Ile Pro Lys Ser His Ser Leu Gly Val Lys
 1105 1110 1115 1120
 Cys Leu Met Val Phe Asn Asn Gln Ile Ile Ser Ala Ala Phe Asp Gly
 1125 1130 1135
 Ser Ile Lys Val Trp Glu Trp Gln Ser Lys
 1140 1145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SRQ ID NO:7:

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ATATGAAGAT ABAACATCAT ATTTAAAGTT TGGTTTTTCT ATCAGCATGA GGAAGTGGAA      60
CTATCAGAAAT TAACAARTCA TACAACARTG TCGCAATTA CAAACATCTT ACATGANGGT      120
AAATATATTA GATTTCATA TCGTACATCT CAACACACCT TCGAAATTCG AAGATGTGTA      180
CCATCTGGTA GTGAGGACCA TCGAACTGCA GACACGCAAT TCGACAACTT TAAAGCACGT      240
ATACATTAG CAGATATTCA ATATAAAGTT GGTGATACAT TATATOTTAG AGTTAAAAAA      300
AGTAAACCAA CAAATGATTC ATTATTACCA ACATTAAATA TAGCATTTTT AGATCGGTCA      360
GAACGTGCAA TTAAATGGGA ATATGACCCA TATACTACAA CTGCTCAATG GACCTGTACA      420
GCACATTAG TCAAGGTGA ACCAGTACCA TTTGCTGAAG GTGCATTAG GAAAGCTTAT      480
CATACATTGG ATTTAAGTAA ATCTGGTGCA AGTGGAGAT ATGATCANA GATTGGTAA      540
AAACCAACAC CAGACCATC ATATTTTGAA GATGTAAAGA TGCMAATGAT AGCAAGGAA      600
TGGCACATA AATATAATTC ATTTAAACCT CCABAAAAGA TTGAATTTTT ACAATCATGC      660
TTTTAGAGT TTGTAGATAC AACATCATCA GATTTAATTT GTGACCCACA ACCATATGTA      720
GAAGGACAAAT ATAGAAACTA TAATAATTAAT AGTGGATTCG TTACTAATGA TGAAGCAAT      780
ACACCAAAAT CATTCTCTCA TTTCAATAT HAACATTCGA ATCATCAATT ATTGATTATA      840
GATATTCAAG GTGTTGGTGA TCACTATACA GACCCACAAA TTCATACCTA TGATCGTCTT      900
GGTTTTGGTA TTGGTAATTT GGGTCAAAAA GGTTTTGAAA AGTTTTTAGA TACTCATAAA      960
TGTAAAGCAA TTTGCCAATA TTAAATTTA CATTCAATTA ATCCAAAATC TGAAAAAAGT      1020
GATTGTGGTA CACTACCAAG ACCAGATTTA ATTTCCCTG ATACATCTGA AAGAGATAAT      1080
AATAATAATA ATAATAATA TAATAATTAAT AATAATAATA ATAATAATA TAATAGTAAT      1140
AATAATAATA ATAACAATAG TACTATTCA AATCATTAG TTGAATTTT AAGTGGTAGT      1200
AAGAAAGAA ATGATAGAGA TTGCCCAGT AGACAATTAT TTGTTTCAA TGATGGTAA      1260

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ACATTAATA CAAATAAGA GAGATCANA TCAATATCA TAGATTTANA AAAACAGAA	1320
ATTTATANA ATAATAGAA AAAAGAGAGT ATAATTTGG AACGATAA ATTAATTCAA	1380
ACTATTAAAG GATATCATCT TACATCTCAT TTATGTATTT GTGATAATT ATTAATTACA	1440
GGATGTTGAG ATAATTCAAT TAGATGTAT CATTAATAAA GTCAAAATAT GGAATGTGTT	1500
CAAACCTTCA AAGGTGATGA AGGTCCAGTT GAATCAATTT GTTATAATCA TCAATATTTG	1560
TTTATGTGTT CATCAGATCA TTCAATTAAA GTTTGGGATT TAACCAATT AAGATGTATT	1620
TTTACGTTGG AGGTTCATGA TAAACCTGTC CATACGGTTT TATTGAATGA TAAATATTTG	1680
TTTACGTTGT CTCTGACAA AACTATCANA GTTTGGGATT TGAAAACTTT CCAATGTAAA	1740
TATACCTTTG AAGTCATGC CAGAGCCGTC AAACACTTT GATATCTGG TCAATATTTA	1800
TTTATGTGTT CAAATGATAA AACTATCAAG GTTTGGGATT TGAAAACTTT TCGTTGTAAC	1860
TACACTCTAA AAGGTCTATC TAAATGGGTC ACCACTATCT GTATATTAGG TACCAATCTC	1920
TACAGTGGCT CCTATGATAA AACTATAAGA GTTTGGAAAT TAAAGAGTT AGAATGTTC	1980
GCTACTTTAA GAGGCCATGA TAGATGGGTT GACATATCG TAATTTGTGA TAAATTATTA	2040
TTTACTGCTA GTGACGATAA TACAATTAAA ATTGCGGATT TAGAAACATT AAGATGTAAT	2100
ACAACTTTGG AAGGACATAA TCCAAACCGTT CAATCTTTAG CACTTTGGGA ACATAAAAAA	2160
TGTGTTATTA GTTGTAGTCA TATCABAAT ATTAGAGTT GGGGTGGAA TTAATTTAAA	2220
ATAAAAAAAA AAAACAT	2237

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (a) ORGANISM: Dictyostelium discoideum

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(x1) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ile	Phe	Lys	Val	Trp	Phe	Ser	Tyr	Glu	Asp	Glu	Glu	Val	Glu	Leu	1	5	10	15
Ser	Glu	Leu	Thr	Asn	Asp	Thr	Thr	Val	Ser	Ala	Ile	Arg	Lys	Ile	Leu	20	25	30	
His	Glu	Gly	Lys	Ile	Phe	Arg	Phe	Pro	Tyr	Gly	Thr	Ser	Gln	Thr	Asp	35	40	45	
Leu	Gln	Ile	Gly	Lys	Met	Leu	Pro	Ser	Gly	Ser	Gly	Gly	Gly	Ala	Thr	50	55	60	
Ala	Asp	Ser	Lys	Phe	Glu	Lys	Phe	Lys	Ala	Arg	Asn	Thr	Leu	Ala	Asp	65	70	75	80
Ile	Gln	Tyr	Lys	Val	Gly	Asp	Thr	Leu	Tyr	Val	Arg	Val	Lys	Lys	Ser	85	90	95	
Lys	Pro	Thr	Asn	Asp	Ser	Leu	Leu	Pro	Thr	Leu	Asn	Ile	Ala	Phe	Leu	100	105	110	
Asp	Gly	Ser	Gln	Arg	Ala	Ile	Lys	Trp	Glu	Tyr	Asp	Pro	Tyr	Thr	Thr	115	120	125	
Thr	Ala	Gln	Trp	Thr	Cys	Thr	Ala	Thr	Leu	Val	Lys	Val	Glu	Pro	Val	130	135	140	
Pro	Phe	Ala	Glu	Gly	Ala	Phe	Arg	Lys	Ala	Tyr	His	Thr	Leu	Asp	Leu	145	150	155	160
Ser	Lys	Ser	Gly	Ala	Ser	Gly	Arg	Tyr	Val	Ser	Lys	Ile	Gly	Lys	Lys	165	170	175	
Pro	Thr	Pro	Arg	Pro	Ser	Tyr	Phe	Glu	Asp	Val	Lys	Met	Gln	Met	Ile	180	185	190	
Ala	Lys	Lys	Trp	Ala	Asp	Lys	Tyr	Asn	Ser	Phe	Lys	Pro	Pro	Lys	Lys	195	200	205	
Ile	Glu	Phe	Leu	Gln	Ser	Cys	Val	Leu	Glu	Phe	Val	Asp	Arg	Thr	Ser	210	215	220	
Ser	Asp	Leu	Ile	Cys	Gly	Ala	Glu	Pro	Tyr	Val	Glu	Gly	Gln	Tyr	Arg	225	230	235	240
Lys	Tyr	Asn	Asn	Asn	Ser	Gly	Phe	Val	Ser	Asn	Asp	Glu	Arg	Asn	Thr	245	250	255	
Pro	Gln	Ser	Phe	Ser	His	Phe	Thr	Tyr	Glu	His	Ser	Asn	His	Gln	Leu				

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	260		265		270
Leu Ile Ile Asp Ile Gln Gly Val Gly Asp His Tyr Thr Asp Pro Gln	275		280		285
Ile His Thr Tyr Asp Gly Val Gly Phe Gly Ile Gly Asn Leu Gly Gln	290		295		300
Lys Gly Phe Glu Lys Phe Leu Asp Thr His Lys Cys Asn Ala Ile Cys	305		310		315
Glu Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp	325		330		335
Cys Gly Thr Val Pro Arg Pro Asp Leu Ile Phe Pro Asp Thr Ser Glu	340		345		350
Arg Asp Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn	355		360		365
Asn Asn Asn Asn Asn Ser Asn Asn Asn Asn Asn Asn Asn Ser Ser Ile	370		375		380
Ser Lys Ser Leu Val Glu Ile Ser Ser Gly Ser Lys Glu Arg Asn Asp	385		390		395
Arg Asp Ser Pro Ser Arg Gln Leu Phe Val Ser Asn Asp Gly Asn Thr	405		410		415
Leu Asn Thr Asn Lys Glu Arg Ser Lys Ser Lys Ser Ile Asp Leu Glu	420		425		430
Lys Pro Glu Ile Leu Ile Asn Asn Lys Lys Lys Glu Ser Ile Asn Leu	435		440		445
Glu Thr Ile Lys Leu Ile Glu Thr Ile Lys Gly Tyr His Val Thr Ser	450		455		460
His Leu Cys Ile Cys Asp Asn Leu Leu Phe Thr Gly Cys Ser Asp Asn	465		470		475
Ser Ile Arg Val Tyr Asp Tyr Lys Ser Gln Asn Met Glu Cys Val Gln	485		490		495
Thr Leu Lys Gly His Glu Gly Pro Val Glu Ser Ile Cys Tyr Asn Asp	500		505		510
Glu Tyr Leu Phe Ser Gly Ser Ser Asp His Ser Ile Lys Val Trp Asp	515		520		525
Leu Lys Lys Leu Arg Cys Ile Phe Thr Leu Gln Gly His Asp Lys Pro					

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530	535	540
Val His Thr Val Leu Leu Asn Asp Lys Tyr Leu Phe Ser Gly Ser Ser		
545	550	555 560
Asp Lys Thr Ile Lys Val Trp Asp Leu Lys Thr Leu Glu Cys Lys Tyr		
	565	570 575
Thr Leu Glu Ser His Ala Arg Ala Val Lys Thr Leu Cys Ile Ser Gly		
	580	585 590
Gln Tyr Leu Phe Ser Gly Ser Asn Asp Lys Thr Ile Lys Val Trp Asp		
	595	600 605
Leu Lys Thr Phe Arg Cys Asn Tyr Thr Leu Lys Gly His Thr Lys Trp		
	610	615 620
Val Thr Thr Ile Cys Ile Leu Gly Thr Asn Leu Tyr Ser Gly Ser Tyr		
	625	630 635 640
Asp Lys Thr Ile Arg Val Trp Asn Leu Lys Ser Leu Glu Cys Ser Ala		
	645	650 655
Thr Leu Arg Gly His Asp Arg Trp Val Glu His Met Val Ile Cys Asp		
	660	665 670
Lys Leu Leu Phe Thr Ala Ser Asp Asp Asn Thr Ile Lys Ile Trp Asp		
	675	680 685
Leu Glu Thr Leu Arg Cys Asn Thr Thr Leu Glu Gly His Asn Ala Thr		
	690	695 700
Val Gln Cys Leu Ala Val Trp Glu Asp Lys Lys Cys Val Ile Ser Cys		
	705	710 715 720
Ser His Asp Gln Ser Ile Arg Val Trp Gly Trp Asp		
	725	730

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATCACCGATCG	ACACACACAAA	TAACACACAC	ATAGTCCAA	CTACTCCACC	AGGATTCCAG	60
CCCTCCGCTC	GCACATTCTC	GCTCAATGCG	TCAAAATGG	TTCGGATAAC	CGACCGACTAC	120
GCAGATGAA	TGTTCAATGA	ACAGAAATGAT	GTGTTTATCG	AGAAGCCTCG	TATGGATCCT	180
CTCCACCTTA	GAAACTTAT	GGAGACATGG	CGCAAGGCTC	CTCCCGAGC	AGGACCAAC	240
TATATACATC	CATGGGATGA	GTTCACATC	CACGATATC	CAGTACAAAG	AGCTAALCGA	300
TATAGGTATT	CTGCATCCAG	AAGCAATGG	ACAGAGGATA	TACACGATGT	GAGACTTCAT	360
CCGGACAGTT	TTGCACGTGG	AGCAATGCGA	GAATGCTACC	GACTCAAAA	CTCCCTCCAG	420
CACGGACAA	GTCAAGATTG	GAGGAGCAAC	TATGTGCGAA	AAGATACAT	TTCTCAAGTC	480
GATCGTAGAG	TTCTTTTCSA	TGATGTGAGA	CTTCAGATGG	ATGCCAAATT	ATGCGCTGAA	540
GAATATAATC	GGTATATTC	AUCCACAAA	ATTGATATTG	TTCAATGTG	TGTCATTGAG	600
ATGATTGATG	TAAACGTTG	TCCACTCTAT	CATTGGAGC	ATTTCATCGA	GGGAAATAT	660
ATAAAATACA	ATTGCAACTC	AGGATTTGTA	TCAATCCAG	CTCGTCTTAC	ACCACAAACA	720
TTTTCTCACP	TCACCTTSHA	ACGTTCTGHT	CATCAAAATCA	TGCTGTGCGA	TATTCAAGGA	780
GTTCGTGATC	TTTACACAGA	TCTTCNGATT	CATACATTTG	TGCAAACTCA	TTATCCAGAT	840
GGAAACCTCC	GAACCTCGTG	ATGGGCTCTT	TTCTTCCATT	CACACAGATG	TAAOCATATT	900
TGTHAGACAA	TGGATCTATC	AAATTTGGA	CTTTCGCCAC	CTGAAATCGA	GGCTACCGAA	960
GTTCAGATGG	AGTAGCTGC	AAAGCAGGAA	AGTCATGCA	TAGTTCTCTC	AACATGCTTC	1020
GAAGCAAGAA	GAAATCGAAT	TTCAAGTGAA	TGTGTACATG	TCGAGCATGG	TATTTGATG	1080
GATCAATTGA	GAAAGAGGAA	GAATTTGAAT	CAATCGTCAA	CCGATTGGTC	AGCAAGAGAT	1140
CACAACGAAG	ACTGTGTATG	TGTTGAGTGT	ATTCCAGTTG	TTGAGCAACT	CTGTGAGGCT	1200
TGCTCCGAG	ATGAGAGGGA	CGAAGAGAG	GACTATCCAA	GAGTGAAAA	AAGTGGAAT	1260
AGTCAGAAA	GTGACCTAG	TAGAATGAGC	ATTTCAGCGA	GATTTTGTGG	CGATGAATCA	1320
GCATCTCGTC	CTACAAAATG	CGGATTTGTA	GATTTAAACT	CACTTCCCTCA	GAGACATGAT	1380

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AGCTTCAGAA GTTCTCTTCC GACATATTCT ATCAATAGTT CTAGACAAAC CAGAGACACT	1440
GAAAAGCATT AATTCTGAAA GGTCTCTTCA AAACAATCAG TTCCAGCAAA CATTCATCA	1500
CTTCAACTTC AACAAATGK TGTTAACCTG GAAATCATT AAGAATGACC ACNAGTCACC	1560
GGGCATCAAT TCTCTCTCTT CGGTCAAGAT CATATTGATE TCTCAUGATA TCATGAGCTC	1620
GGGCGCTTCC TAGAATTTRA TTCAGAACAT AAGGAAATGC TTGAGGCGAG TCAAAATGAC	1680
GCTGCTGTAC CAATCAATA CGACAAGCAG TCTGCAATTT TCCATTTCGA TATCGCTCGG	1740
AAGTGTGGAA TCCTTGAGGC TGTGCTAACA TCGGCTCATA TTGTTCTCGG ATTACACAT	1800
CAATTTCTTA AAGAGTCAC CGTTGATGAT CTGTTTCTTA ATGGGTTTGG AGAAGAGCAA	1860
AATCAATTTC GAGCTGATAA AGGACNVAAA CCTTGTGACC TAGAAGAGTT CGGCTTCGAT	1920
CTGATGAAA TTGCTGCGA GATGGGTGAT AAGGGTGCAA TGCTGTACAT GGCACACGCT	1980
TATGAACTC CTCAGCATCT CGGACCGAAT CGAAGAACGG ATTATAGAA ATCGATTGAT	2040
TGSTATCABC GCGTGGTTGG ATTCCAGGAA GAGGAAAGAC TTCACTCTGA TTGTGGAAAA	2100
ACGACATTCT CCGCATTTGC TCGACTGACT CGTCACGAAA TTTTAGCCAA AATCGCTGAA	2160
ATGTACAAAG AGGCACCTTA TGGCTTAAAT CAAGACTTCG AAGGAGCATA TGGTCTATTG	2220
AATGAAGCTG CTGAAGCACC AATGGAGGCA ATGAATGGA AGCTGCGAAA TAATACTAT	2280
GAAAAGCGG AATGTCTCC AGAATGA	2307

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 768 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *C. elegans*

(x) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
 1 5 10 15
 Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
 20 25 30
 Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
 35 40 45
 Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
 50 55 60
 Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
 65 70 75 80
 Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
 85 90 95
 Arg Ala Lys Arg Tyr Arg Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
 100 105 110
 Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
 115 120 125
 Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
 130 135 140
 Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
 145 150 155 160
 Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys
 165 170 175
 Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp
 180 185 190
 Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro
 195 200 205
 Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
 210 215 220
 Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala
 225 230 235 240
 Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Glu Met Met Val Val
 245 250 255
 Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His Thr
 260 265 270

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Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu Gly Thr Arg Gly Met
 275 280 285
 Ala Leu Phe Phe His Ser His Arg Cys Asn Asp Ile Cys Glu Thr Met
 290 295 300
 Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu Ile Glu Ala Thr Glu
 305 310 315 320
 Val Ala Met Glu Val Ala Ala Lys Glu Lys Lys Ser Cys Ile Val Pro
 325 330 335
 Pro Thr Val Phe Glu Ala Arg Arg Asn Arg Ile Ser Ser Glu Cys Val
 340 345 350
 His Val Glu His Gly Ile Ser Met Asp Glu Leu Arg Lys Arg Lys Thr
 355 360 365
 Leu Asn Glu Ser Ser Thr Asp Leu Ser Ala Lys Ser His Asn Glu Asp
 370 375 380
 Cys Val Cys Pro Glu Cys Ile Pro Val Val Glu Glu Leu Cys Glu Pro
 385 390 395 400
 Cys Ser Glu Asp Glu Glu Asp Glu Glu Glu Asp Tyr Pro Arg Ser Glu
 405 410 415
 Lys Ser Gly Asn Ser Glu Lys Ser Arg Arg Ser Arg Met Ser Ile Ser
 420 425 430
 Thr Arg Ser Ser Gly Asp Glu Ser Ala Ser Arg Pro Arg Lys Cys Gly
 435 440 445
 Phe Val Asp Leu Asn Ser Leu Arg Glu Arg His Asp Ser Phe Arg Ser
 450 455 460
 Ser Val Gly Thr Tyr Ser Met Asn Ser Ser Arg Glu Thr Arg Asp Thr
 465 470 475 480
 Glu Lys Asp Glu Phe Trp Lys Val Leu Arg Lys Glu Ser Val Pro Ala
 485 490 495
 Asn Ile Leu Ser Leu Glu Leu Glu Glu Met Ala Ala Asn Leu Glu Asn
 500 505 510
 Asp Glu Asp Val Pro Glu Val Thr Gly His Glu Phe Ser Val Leu Gly
 515 520 525
 Glu Ile His Ile Asp Leu Ser Arg Tyr His Glu Leu Gly Arg Phe Val
 530 535 540

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Glu Val Asp Ser Gln His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp	
545	550 555 560
Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu	
	565 570 575
Asp Ile Ala Arg Lys Cys Gly Ile Leu Glu Ala Val Leu Thr Ser Ala	
	580 585 590
His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val	
	595 600 605
Asp Asp Leu Phe Pro Asn Gly Phe Gly Glu Gln Glu Asn Gly Ile Arg	
	610 615 620
Ala Asp Lys Gly Gln Lys Pro Cys Asp Leu Glu Glu Phe Gly Ser Asp	
	625 630 635 640
Asp Met Glu Ile Ala Ala Glu Met Gly Asp Lys Gly Ala Met Leu Tyr	
	645 650 655
Met Ala His Ala Tyr Glu Thr Gly Gln His Leu Gly Pro Asn Arg Arg	
	660 665 670
Thr Asp Tyr Lys Lys Ser Ile Asp Thr Tyr Gln Arg Val Val Gly Phe	
	675 680 685
Gln Gln Gln Glu Glu Leu Asp Ser Asp Cys Gly Lys Thr Thr Phe Ser	
	690 695 700
Ser Phe Ala Pro Leu Thr Arg His Glu Ile Leu Ala Lys Met Ala Glu	
	705 710 715 720
Met Tyr Lys Gln Gly Gly Tyr Gly Leu Asn Gln Asp Phe Glu Arg Ala	
	725 730 735
Tyr Gly Leu Phe Asn Glu Ala Ala Glu Ala Ala Met Glu Ala Met Asn	
	740 745 750
Gly Lys Leu Ala Asn Lys Tyr Tyr Glu Lys Ala Glu Met Cys Gly Gln	
	755 760 765

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

ATGACGATCG ACACAACGAA TGAGAGCGGAC AATAGTCCAA CTAACTCACC ACGATTGGAG      60
GCTCTGGGCTC GGACATTCTC GCTCAATGCC TCAGAAATGG TTGGGATAAC CGACGACTAC      120
GCAGATGAAC TTCTCATTGA ACAGAATGAT GTCGTTATCG AGAAGCCTCG TATGGATCCT      180
CTCCACCTTA GAAAACTTAT GGAGCATGG CGCAGGCTT CTCCCGGAGC AAGAACAAC      240
TATATAGATT CATGGGATGA GTTCACATC CACGAGTATC CACTACAACG ACCTAAGCGA      300
TATAGTTATT CTGCATCAG AAAGCAATGG ACAGAGGATA TACTTGATTT GAGACTTCAT      360
CGGACAGTT TTGCACGTGG AGCCATCGA GAATGCTACC GACTCAAAA GTGCTCCAG      420
CACCGACAA GTCAAGATTG GAGCAGCAAC TAGTTCGCA AAGATACAT TTGTCAAGTC      480
GATCGTAGAG TTCTTTTCGA TGATGTCAGA CTTCAGATGG ATGCCAATT ATGGGCTGAA      540
GAATATATC GGTATAATCC ACUGAAGAAA ATTGATATTG TTCAAATGG TGTCATTGAG      600
ATGATTGATG TAAAGGTTT TCCACTCTAT CATTTCGAGC ATTCATCGA GGGAAATAT      660
ATAAATACA ATTCAAACTC AGGATTTGTA TCBAATCCAG CTCTCTTAC ACCACAAGCA      720
TTTTCTCACT TCACCTTCCA AGTTTCTGAT CATCAAAATCA TGGTTGTGTA TATTCAGGA      780
GTTGGTGATC TTACACACA TCTCTAGATT CATACATTC TCGCAACTGA TTATGGAGAT      840
GGAAACCTCG GAACTCTGCG AATGGCTCTT TTCTTCATT CACACACATG TAAGGATATT      900
TGTGAGACAA TGGATCTATC AATTTTCGAA CTTCGGCAC CTGAAATCGA CGCTACCGAA      960
GTTCCGATCC AATTAGCTGC AAGCGAGAAA AAGTCATGCA TATTCTCTTC AACTCTCTTC      1020
GAAGCAAGAA GAAATCGAAT TTCAGTGAA TGTGTACATG TCGAGCATGG TATTTGATG      1080
GATCAATTGA GAAAGAGGAA GACCTTCGAT CAATCTTCAA CGGATTTGTC AGCNAAGAGT      1140
CACACGAAG ACTGTGTATG TCTCACTCT ATTCCAGTTG TTGAGCAACT CTGTGAGCCT      1200

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TGCCTCCGAAG ATCAGACAGCA CCGAGGAGAA GACTATCCAA GAAGTGAAAH AAGTGGGAAT 1260
AGTCACAGAA CTCCAGCTAG TAGATGAAK ATTTCAAGCA CATCTTCTGG CGATGAATCA 1320
CGATCTCCTC CTACAAATG CGAATTTGTA GATTTAAGCT CACTCTGTC GAGACATGAT 1380
AGCTTCAGAA GTTCTGTGG GACATATTCT AGAATAGTT CTACACAAAC CAGAGAACT 1440
GAAAGGATG AATTCTGGAA GGTTCCTCGA AAACAATCAG TTCCAGCAA CATTCTATCA 1500
CTTCAACTTC AACAAATGGC TGTAACTCTG CAAATGATG AAGAGGTACC ACAAGTCACC 1560
GGGCATCAGT TCTCTGTCT CGGTACAGAT CATATGATC TCTACGATA TCATGAGCTC 1620
GGGCGGTTCC TAGAAGTTGA TTACAGACAT AAGGAAATGC TTGAGGGAG TGAAATGAC 1680
GCTCGTGATC CAATCAATA CCACAGCCAC TCTGCAATT TCCATTGGA TATCGCTCGG 1740
AAGTGTGGAA TCCITCAAGC TGTGCTAACA TGTGCTCATA TTCTTCTGG ATTACCACAT 1800
CAATTCTTGA AAGAAATCAC CGTTGATGAT CTGTTTCTA ATGAGTTTTC AGAACAGGA 1860
AATGGAATTC GAGACCTAGA AGAGTTCCGC TCCGATCTGA TGGAAATTGC TACAGAGATC 1920
CGTCATAAGC GTTCAATGCT GTACATGGCA CAGCTTATG AACTGGTCA GATCTCCCA 1980
CCCAATCCAA CAGCAGATTA TAGAATTCG ATTGATTGGT ATCAACGCGT CGTTGCAATC 2040
CAGCAGAAAG AAGAACTTGA CTCTGATTGT GGAAGAACGA CATTCTCTC ATTTGCTCCA 2100
CTGACTCGTC ACCGATTTCT AGCCAAATG GCTGAAATGT ACAAGAGGG AGGTTATGGC 2160
CTGAATCAAG ACTTCGAACG AGCATAATGT CTATTCAATG AAGCTTCTGA AGCAGCAATG 2220
GAGCAATGA ATGGAAGCT CGCAAAATAA TACTATGAA AAGCCCAAT CTCTCCAGAA 2280
TGA 2383

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ORIGINAL SOURCE:

-31-

(A) ORGANISM: *C. elegans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Thr Ile Asp Thr Thr Asn Glu Ser Asp Asn Ser Pro Thr Asn Ser
1           5           10           15

Pro Gly Leu Glu Ala Ser Ala Arg Thr Phe Ser Leu Asn Ala Ser Lys
20           25           30

Met Val Arg Ile Thr Asp Asp Tyr Ala Asp Glu Val Phe Ile Glu Gln
35           40           45

Asn Asp Val Val Ile Glu Lys Pro Arg Met Asp Pro Leu His Val Arg
50           55           60

Lys Leu Met Glu Thr Trp Arg Lys Ala Ala Arg Arg Ala Arg Thr Asn
65           70           75           80

Tyr Ile Asp Pro Trp Asp Glu Phe Asn Ile His Glu Tyr Pro Val Gln
85           90           95

Arg Ala Lys Arg Tyr Arg Tyr Ser Ala Ile Arg Lys Gln Trp Thr Glu
100          105          110

Asp Ile Val Asp Val Arg Leu His Pro Asp Ser Phe Ala Arg Gly Ala
115          120          125

Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser Lys His Gly Thr Ser
130          135          140

Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg Tyr Ile Cys Gln Val
145          150          155          160

Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu Gln Met Asp Ala Lys
165          170          175

Leu Trp Ala Glu Gln Tyr Asn Arg Tyr Asn Pro Pro Lys Lys Ile Asp
180          185          190

Ile Val Gln Met Cys Val Ile Glu Met Ile Asp Val Lys Gly Ser Pro
195          200          205

Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
210          215          220

Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg Leu Thr Pro Gln Ala
225          230          235          240

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Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	Ser	Gly	His	Gln	Met	Met	Val	Val		
				245					250					255			
Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	Tyr	Thr	Asp	Pro	Gln	Ile	His	Thr		
			260					265					270				
Val	Val	Gly	Thr	Asp	Tyr	Gly	Asp	Gly	Asn	Leu	Gly	Thr	Arg	Gly	Met		
		275					280					285					
Ala	Leu	Phe	Phe	His	Ser	His	Arg	Cys	Asn	Asp	Ile	Cys	Glu	Thr	Met		
	290					295					300						
Asp	Leu	Ser	Asn	Phe	Glu	Leu	Ser	Pro	Pro	Glu	Ile	Glu	Ala	Thr	Glu		
305					310					315					320		
Val	Ala	Met	Glu	Val	Ala	Ala	Lys	Gln	Lys	Lys	Ser	Cys	Ile	Val	Pro		
			325					330						335			
Pro	Thr	Val	Phe	Gln	Ala	Arg	Arg	Asn	Arg	Ile	Ser	Ser	Glu	Cys	Val		
			340					345					350				
His	Val	Glu	His	Gly	Ile	Ser	Met	Asp	Gln	Leu	Arg	Lys	Arg	Lys	Thr		
		355					360					365					
Leu	Asn	Gln	Ser	Ser	Thr	Asp	Leu	Ser	Ala	Lys	Ser	His	Asn	Gln	Asp		
	370					375					380						
Cys	Val	Cys	Pro	Gln	Cys	Ile	Pro	Val	Val	Gln	Gln	Leu	Cys	Glu	Pro		
385					390					395					400		
Cys	Ser	Gln	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Tyr	Pro	Arg	Ser	Glu		
			405						410				415				
Lys	Ser	Gly	Asn	Ser	Gln	Lys	Ser	Arg	Arg	Ser	Arg	Met	Ser	Ile	Ser		
			420					425					430				
Thr	Arg	Ser	Ser	Gly	Asp	Gln	Ser	Ala	Ser	Arg	Pro	Arg	Lys	Cys	Gly		
	435					440						445					
Phe	Val	Asp	Leu	Asn	Ser	Leu	Arg	Gln	Arg	His	Asp	Ser	Phe	Arg	Ser		
	450					455					460						
Ser	Val	Gly	Thr	Tyr	Ser	Met	Asn	Ser	Ser	Arg	Gln	Thr	Arg	Asp	Thr		
465					470					475					480		
Glu	Lys	Asp	Glu	Phe	Trp	Lys	Val	Leu	Arg	Lys	Gln	Ser	Val	Pro	Ala		
			485						490					495			
Asn	Ile	Leu	Ser	Leu	Gln	Leu	Gln	Gln	Met	Ala	Ala	Asn	Leu	Glu	Arg		
			500					505					510				

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Asp Glu Asp Val Pro Gln Val Thr Gly His Gln Phe Ser Val Leu Gly
 515 520 525
 Gln Ile His Ile Asp Leu Ser Arg Tyr His Glu Leu Gly Arg Phe Val
 530 535 540
 Glu Val Asp Ser Gln His Lys Glu Met Leu Glu Gly Ser Glu Asn Asp
 545 550 555 560
 Ala Arg Val Pro Ile Lys Tyr Asp Lys Gln Ser Ala Ile Phe His Leu
 565 570 575
 Asp Ile Ala Arg Lys Cys Gly Ile Leu Gln Ala Val Leu Thr Ser Ala
 580 585 590
 His Ile Val Leu Gly Leu Pro His Glu Leu Leu Lys Glu Val Thr Val
 595 600 605
 Asp Asp Leu Phe Pro Asn Gly Phe Gly Gln Gln Gln Asn Gly Ile Arg
 610 615 620
 Asp Leu Glu Gln Phe Gly Ser Asp Leu Met Glu Ile Ala Ala Glu Met
 625 630 635 640
 Gly Asp Lys Gly Ala Met Leu Tyr Met Ala His Ala Tyr Glu Thr Gly
 645 650 655
 Gln His Leu Gly Pro Asn Arg Arg Thr Asp Tyr Lys Lys Ser Ile Asp
 660 665 670
 Trp Tyr Gln Arg Val Val Gly Phe Gln Glu Gln Gln Glu Leu Asp Ser
 675 680 685
 Asp Cys Gly Lys Thr Thr Phe Ser Ser Phe Ala Pro Leu Thr Arg His
 690 695 700
 Glu Ile Leu Ala Lys Met Ala Glu Met Tyr Lys Glu Gly Gly Tyr Gly
 705 710 715 720
 Leu Asn Gln Asp Phe Gln Arg Ala Tyr Gly Leu Phe Asn Glu Ala Ala
 725 730 735
 Gln Ala Ala Met Glu Ala Met Asn Gly Lys Leu Ala Asn Lys Tyr Tyr
 740 745 750
 Glu Lys Ala Glu Met Cys Gly Glu
 755 760

(2) INFORMATION FOR SEQ ID NO:13:

(1) SEQUENCE CHARACTERISTICS:

-34-

(A) LENGTH: 638 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTATTGTATG TTTTCAATT GAGAAGACTC CATTTCGAAA GGGTAGTTGT AGAACAGCAC	60
ATAAAATTAAA GATTGGAGT CAACCAATC AAGGATTAGT TGATAAATTT TCAACCAATA	120
AAAAGAGGAC AAGAGATTCA TACTTTACAG ATGTATTGAT GCAACATTT TGTGCTAAAT	180
GGGCAGAGAA ATTCAATGAA CGGAGAGCAC CAAAACCAAT TACATTCTTA CCATCATACG	240
TTTACGAATT GATTGATCAT CCACCAAGCT ATCCACTTTC TGGTGGTGAA CCATTCAATG	300
AGGGAGATTA CAGGAACAT AACACACACA GTGCTTACGT TACTAGTGAT GCTAGAAATA	360
CACCAACATC ATTCTTCAT TTCTCATAAG AACTCTCCAA TCATCAATTG TTGATGTTG	420
ATATCCAAAG TGTCAACCAT TTCTACCTG ATCCTCAAT TCATACGAAA TCAGCCACAG	480
GCTTTGGCEA GGGTAATTTG GCGAGACCG GTTCCACAA ATTCTTCAA ACACACAAGT	540
GTAATCCACT TTTGACTTT TTAAGTTGA AAUCAATCAA TCATCAAG AAAGCCCTCC	600
TACAGGTAC ATTACCGTC GTACAAT	628

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

-35-

(A) ORGANISM: Dictyostelium discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Ile Val Cys Val Ser Ile Glu Lys Thr Pro Phe Ala Lys Gly Ser Cys
1           5           10           15

Arg Thr Ala His Lys Leu Lys Asp Trp Ser Gln Pro Asp Gln Gly Leu
20           25           30

Val Gly Lys Phe Ser Thr Asn Lys Lys Thr Thr Arg Asp Ser Tyr Phe
35           40           45

Thr Asp Val Leu Met Gln Thr Phe Cys Ala Lys Trp Ala Glu Lys Phe
50           55           60

Asn Glu Ala Lys Pro Pro Lys Pro Ile Thr Phe Leu Pro Ser Tyr Val
65           70           75           80

Tyr Glu Leu Ile Asp His Pro Pro Pro Tyr Pro Val Cys Gly Gly Glu
85           90           95

Pro Phe Ile Glu Gly Asp Tyr Lys Lys His Asn Asn Asn Ser Gly Tyr
100          105          110

Val Ser Ser Asp Ala Arg Asn Thr Pro Gln Ser Phe Ser His Phe Ser
115          120          125

Tyr Glu Leu Ser Asn His Glu Leu Leu Ile Val Asp Ile Gln Gly Val
130          135          140

Asn Asp Phe Tyr Thr Asp Pro Gln Ile His Thr Lys Ser Gly Glu Gly
145          150          155          160

Phe Gly Glu Gly Asn Leu Gly Glu Thr Gly Phe His Lys Phe Leu Gln
165          170          175

Thr His Lys Cys Asn Pro Val Cys Asp Phe Leu Lys Leu Lys Pro Ile
180          185          190

Asn Gln Ser Lys Lys Ala Leu Leu Arg Gly Thr Leu Pro Val Val Gln
195          200          205

Leu

```

(2) INFORMATION FOR SEQ ID NO:15:

(1) SEQUENCE CHARACTERISTICS:

-36-

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly	Glu	Trp	Ileu	Asp	Asp	Glu	Val	Leu	Ile	Lys	Met	Ala	Ser	Gln	Pro	1	5	10	15
Phe	Gly	Arg	Gly	Ala	Met	Arg	Glu	Cys	Phe	Arg	Thr	Lys	Lys	Leu	Ser	20	25	30	
Asn	Phe	Leu	His	Ala	Gln	Gln	Trp	Lys	Gly	Ala	Ser	Asn	Tyr	Val	Ala	35	40	45	
Lys	Arg	Tyr	Ile	Glu	Pro	Val	Asp	Arg	Asp	Val	Tyr	Phe	Glu	Asp	Val	50	55	60	
Arg	Leu	Gln	Met	Glu	Ala	Lys	Leu	Trp	Gly	Glu	Glu	Tyr	Asn	Arg	His	65	70	75	80
Lys	Pro	Pro	Lys	Gln	Val	Asp	Ile	Met	Gln	Met	Cys	Ile	Ile	Glu	Leu	85	90	95	
Lys	Asp	Arg	Pro	Gly	Lys	Pro	Leu	Phe	His	Leu	Glu	His	Tyr	Ile	Glu	100	105	110	
Gly	Lys	Tyr	Ile	Lys	Tyr	Asn	Ser	Asn	Ser	Gly	Phe	Val	Arg	Asp	Asp	115	120	125	
Asn	Ile	Arg	Leu	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Phe	Glu	Arg	130	135	140	
Ser	Gly	His	Gln	Ileu	Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Gly	Asp	Leu	145	150	155	160
Tyr	Thr	Asp	Pro	Gln	Ile	His	Thr	Glu	Thr	Gly	Thr	Asp	Phe	Gly	Asp	165	170	175	
Gly	Asn	Leu	Gly	Val	Arg	Gly	Met	Ala	Leu	Phe	Phe	Tyr	Ser	His	Ala	180	185	190	

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Cys Asn Arg Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser
195 200 205

Pro Arg Glu Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser
210 215 220

Ala Lys Thr Ile Leu Arg Gly Thr Glu Glu Lys Cys Gly Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: D. discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Lys Trp Ile Arg Leu Ser Met Lys Leu Lys Val Glu Arg Lys Pro
1 5 10 15

Phe Ala Glu Gly Ala Leu Arg Glu Ala Tyr His Thr Val Ser Leu Gly
20 25 30

Val Gly Thr Asp Glu Asn Tyr Pro Leu Gly Thr Thr Thr Lys Leu Phe
35 40 45

Pro Pro Ile Glu Met Ile Ser Pro Ile Ser Lys Asn Asn Glu Ala Met
50 55 60

Thr Glu Leu Lys Asn Gly Thr Lys Phe Val Leu Lys Leu Tyr Lys Lys
65 70 75 80

Glu Ala Glu Gln Gln Ala Ser Arg Glu Leu Tyr Phe Glu Asp Val Lys
85 90 95

Met Gln Met Val Cys Arg Asp Trp Gly Asn Lys Phe Asn Gln Lys Lys
100 105 110

Pro Pro Lys Lys Ile Glu Phe Leu Met Ser Trp Val Val Glu Leu Ile
115 120 125

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Asp	Arg	Ser	Pro	Ser	Ser	Asn	Gly	Glu	Pro	Ile	Leu	Cys	Ser	Ile	Glu
130						135					140				
Pro	Leu	Leu	Val	Gly	Glu	Phe	Lys	Lys	Asn	Asn	Ser	Asn	Tyr	Gly	Ala
145				150					155						160
Val	Leu	Thr	Asn	Arg	Ser	Thr	Pro	Gln	Ala	Phe	Ser	His	Phe	Thr	Tyr
			165					170					175		
Glu	Leu	Ser	Asn	Lys	Gln	Met	Ile	Val	Val	Asp	Ile	Gln	Gly	Val	Asp
		180					185					190			
Asp	Leu	Tyr	Thr	Asp	Pro	Gln	Ile	His	Thr	Pro	Asp	Gly	Lys	Gly	Phe
195						200						205			
Gly	Leu	Gly	Asn	Leu	Gly	Lys	Ala	Gly	Ile	Asn	Lys	Phe	Ile	Thr	Thr
210					215						220				
His	Lys	Cys	Asn	Ala	Val	Cys	Ala	Leu	Leu	Asp	Leu	Asp	Val	Lys	Leu
225				230						235					240
Gly	Gly	Val	Leu	Ser	Gly	Asn	Asn	Lys	Lys	Gln	Leu	Gln	Gln	Gly	Thr
			245					250						255	
Met	Val														

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ORIGINAL SOURCE:

- (A) ORGANISM: D. discoideum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala	Gln	Trp	Thr	Cys	Thr	Ala	Thr	Leu	Val	Lys	Val	Glu	Pro	Val	Pro
1				5					10					15	
Phe	Ala	Gln	Gly	Ala	Phe	Arg	Lys	Ala	Tyr	His	Thr	Leu	Asp	Leu	Ser
		20					25						30		

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Lys Ser Gly Ala Ser Gly Arg Tyr Val Ser Lys Ile Gly Lys Lys Pro
 35 40 45
 Thr Pro Arg Pro Ser Tyr Phe Glu Asp Val Lys Met Gln Met Ile Ala
 50 55 60
 Lys Lys Trp Ala Asp Lys Tyr Asn Ser Phe Lys Pro Pro Lys Lys Ile
 65 70 75 80
 Glu Phe Leu Gln Ser Cys Val Leu Glu Phe Val Asp Arg Thr Ser Ser
 85 90 95
 Asp Leu Ile Cys Gly Ala Glu Pro Tyr Val Glu Gly Gln Tyr Arg Lys
 100 105 110
 Tyr Asn Asn Asn Ser Gly Phe Val Ser Asn Asp Gln Arg Asn Thr Pro
 115 120 125
 Gln Ser Phe Ser His Phe Thr Tyr Glu His Ser Asn His Gln Leu Leu
 130 135 140
 Ile Ile Asp Ile Gln Gly Val Gly Asp His Tyr Thr Asp Pro Gln Ile
 145 150 155 160
 His Thr Tyr Asp Gly Val Gly Phe Gly Ile Gly Asn Leu Gly Gln Lys
 165 170 175
 Gly Phe Glu Lys Phe Leu Asp Thr His Lys Cys Asn Ala Ile Cys Gln
 180 185 190
 Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp Cys
 195 200 205
 Gly Thr Val Pro
 210

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: C. elegans

-4(-

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Gln Trp Thr Gln Asp Ile Val Asp Val Arg Leu His Pro Asp Ser
 1 5 10 15
 Phe Ala Arg Gly Ala Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser
 20 25 30
 Lys His Gly Thr Ser Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg
 35 40 45
 Tyr Ile Cys Gln Val Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu
 50 55 60
 Gln Met Asp Ala Lys Leu Trp Ala Glu Gln Tyr Asn Arg Tyr Asn Pro
 65 70 75 80
 Pro Lys Lys Ile Asp Ile Val Gln Met Cys Val Ile Glu Met Ile Asp
 85 90 95
 Val Lys Gly Ser Pro Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys
 100 105 110
 Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg
 115 120 125
 Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His
 130 135 140
 Glu Met Met Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
 145 150 155 160
 Pro Gln Ile His Thr Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu
 165 170 175
 Gly Thr Arg Gly Met Ala Leu Phe Phe His Ser His Arg Cys Asn Asp
 180 185 190
 Ile Cys Glu Thr Met Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu
 195 200 205
 Ile Glu Ala Thr Glu Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys
 210 215 220
 Ser Cys Ile Val Pro Pro Thr Val Phe
 225 230

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

-41-

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide Primer D"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATTTCGAC TGGACAAGAA CCCCC

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Arg	Lys	Lys	Phe	Gly	Glu	Ser	Glu	Lys	Thr	Lys	Thr	Lys	Glu	Phe	Leu
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Ala Asn Asn Tyr Tyr Glu Lys Ala Glu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGCGCTTNN NNCAATTNAC NTINGANNG

29

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCGCGCTTTT CNTATTAATT NTTGCG

26

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Oligonucleotides"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACATTCAGC TGATGAUCAA AACGCTC

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(21) International Application Number: PCT/US98/17272 (22) International Filing Date: 20 August 1998 (20.08.98) (30) Priority Data: 08/914,999 20 August 1997 (20.08.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 08/914,999 (CIP) Filed on 20 August 1997 (20.08.97) (71) Applicant (for all designated States except US): UNIVERSITY OF MEDICINE AND DENTISTRY OF NEW JERSEY [US/US]; 30 Bergen Street, Newark, NJ 07107-3000 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): RYAZANOV, Alexey G. [RU/US]; 82 Gulick Road, Princeton, NJ 08540 (US). HAIT, William, N. [US/US]; 61 Overbrook Drive, Princeton, NJ 08540 (US). PAVUR, Karen, S. [US/US]; Apartment C, 68 1/2 Woodbridge Avenue, Highland Park, NJ 08904 (US). (74) Agents: COHEN, Mark, S. et al.; Klauber & Jackson, 411 Hackensack Avenue, Hackensack, NJ 07601 (US).		(81) Designated States: AU, CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 3 June 1999 (03.06.99)
(54) Title: ELONGATION FACTOR-2 KINASE (EF-2 KINASE) AND METHODS OF USE THEREFOR		
(57) Abstract <p>A new superfamily of protein kinases has been discovered that centers around eukaryotic elongation factor-2 kinase (eEF-2 kinase). The protein kinases of this new superfamily have the following characteristics: 1) sequence similarity to eEF-2 kinase; 2) no sequence similarity to the protein kinases of either the serine/threonine/tyrosine kinase or histidine kinase superfamily; and, 3) specifically phosphorylates α-helical regions of proteins as opposed to β-turns, as seen in all other protein kinases. Assays have been developed utilizing eEF-2 kinase and a phosphorylation target consisting of a novel α-helical 16-amino acid peptide sequence to facilitate high-throughput screening for compounds that can specifically inhibit this protein kinase that has been implicated tumor growth and other hyperproliferative disorders. Additionally, the disclosed invention includes assessing eEF-2 kinase levels for diagnostic purposes, and therapeutic formulations to inhibit eEF-2 kinase activity.</p>		

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/17272

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12P21/02 C07K14/00 C07K16/00 C12N15/11 C12N1/11
C12N1/15 C12N1/19 C12N1/21 C12N15/63

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12P C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	W. HAIT ET AL.: "Elongation vfactor-2 kinase: immunological evidence for the existence of tissue specific forms" FEBS LETTERS, vol. 397, 1996, pages 55-60, XP002097685 *see the whole article* ---	1-51
X	G.P. COTE ET AL.: "Mapping of the novel protein kinase catalytic domain of Dictyostelium myosin II heavy chain kinase A" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 272, no. 11, 1997, pages 6846-6849, XP002097686 *see the whole article* --- -/--	1-51

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

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Date of the actual completion of the international search

24 March 1999

Date of mailing of the international search report

20/04/1999

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Marie, A

INTERNATIONAL SEARCH REPORT

Patent Application No

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	S. RAVID ET AL.: "Membrane bound Dictyostelium myosin heavy chain kinase: a developmentally regulated substrate specific member of the protein kinase C family" PNAS, vol. 89, 1992, pages 5877-5881, XP002097687 *see the whole article* ---	1-51
X	L.M. FUTEY ET AL.: "Structural analysis of myosin heavy chain kinase A" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 2, 1995, pages 523-529, XP002097688 *see the whole article* ---	1-51
X	C.E. CLANCY ET AL.: "Identification of a protein kinase from Dictyostelium with homology to the novel catalytic domain of myosin heavy chain kinase A" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 272, no. 18, 1997, pages 11812-11815, XP002097689 *see the whole article* ---	1-51
X	Proceedings of the 88th annual meeting of the american association for cancer research, 1997, 38, abstract 2806 XP002097696 *see the whole abstract* ---	1-51
X	Proceedings of the 88th annual meeting of the american association for cancer research, 1997, 38, abstract 3762 XP002097697 *see the whole abstract* ---	1-51
X	Proceedings of the 88th annual meeting of the american association for cancer research, 1997, 38, abstract 3761 XP002097698 *see the whole abstract* ---	1-51
X	N.T. REDPATH ET AL.: "Cloning and expression of cDNA encoding protein synthesis elongation factor-2 kinase" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 271, no. 29, 1996, pages 17547-17554, XP002097690 *see the whole article* ---	1-51
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INTERNATIONAL SEARCH REPORT

Inter: Application No
PCT/US 98/17272

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	A.G. RYAZANOV ET AL.: "Identification of a new class of protein kinases represented by eukaryotic elongation factor-2 kinase" PNAS, vol. 94, 1997, pages 4884-4889, XP002097691 *see the whole article* ---	1-51
X	K. MITSUI ET AL.: "Purification and characterization of calmodulin dependent protein kinase III from rabbit reticulocytes and rat pancreas" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 268, no. 18, 1993, pages 13422-13433, XP002097692 *see the whole article* ---	1-51
X	N.T. REDPATH ET AL.: "Purification and phosphorylation of elongation factor-2 kinase from rabbit reticulocytes" EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 212, 1993, pages 511-520, XP002097693 *see the whole article* ---	1-51
X	A. GAJKO ET AL.: "Purification and characterization of the protein kinase eEF-2 isolated from rat liver cells" ACTA BIOCHIMICA POLONICA, vol. 41, no. 4, 1994, pages 421-427, XP002097694 *see the whole article* ---	1-51
X	A.C. NAIRN ET AL.: "Calcium/calmodulin dependent protein kinases" CANCER BIOLOGY, vol. 5, 1994, pages 295-303, XP002097695 *see the whole article* -----	1-51

